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Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                               Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                   799.5
768
765
759
                                                                                                                                                                                                                                                                                                                                                  Score
100.0
88.1
88.0
70.6
56.9
54.6
54.4
42.7
42.7
                                                                                                                                                                                                                                                                                                                                                  Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\AA1980.DAT: *
2: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\AA1981.DAT: *
3: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\AA1981.DAT: *
3: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\AA1982.DAT: *
4: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\AA1982.DAT: *
5: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\AA1983.DAT: *
5: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\AA1983.DAT: *
6: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\AA1985.DAT: *
7: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\AA1986.DAT: *
7: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\AA1986.DAT: *
8: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\AA1987.DAT: *
9: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\AA1989.DAT: *
9: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\AA1989.DAT: *
10: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\AA1999.DAT: *
11: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\AA1999.DAT: *
12: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\AA1999.DAT: *
13: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\AA1993.DAT: *
14: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\AA1993.DAT: *
15: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\AA1993.DAT: *
16: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\AA1993.DAT: *
17: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\AA1993.DAT: *
18: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\AA1993.DAT: *
19: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\AA1993.DAT: *
20: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\AA1993.DAT: *
21: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\AA1993.DAT: *
22: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\AA1993.DAT: *
23: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\AA1993.DAT: *
24: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\AA1993.DAT: *
25: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\AA1993.DAT: *
26: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\AA1993.DAT: *
27: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\AA1993.DAT: *
28: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\AA1993.DAT: *
29: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\AA1993.DAT: *
20: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\AA1993.DAT: *
21: \SIDSI\gcgdata\
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                 Query
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MAFEELLSQVGGLGRFQMLH...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A_Geneseq_032802:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maximum Match
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Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                        Length
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22
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                                                                                                                                                                               AAM24188
AAE04897
                                                                                                                                                                                                                                                                  AAY52386
AAB47276
AAM41845
AAE06612
                                                          AAB19406
AAE10332
                                                                                                                                                AAB47275
                                                                                                                                                                                                                                          ABB11732
                                                                                                                     AAM40059
                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
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                                                                                                                                                                                                                                                                                                                                                        Description
                                                                                            Human polypeptide
Amino acid sequenc
                                                                                                                                                                                                                                                                                                 Human transmembran
                                                                                                                                                      hOAT4.
                                                                                                                                                                               Human transporter
                                                                                                                                                                                                                 Human
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                                                                Human
                                                                                                                                                                                                              s. Homo sapie
n secreted pro
n EST encoded
      protein havi
                              transporter polypeptide
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הדהפה ווכדמווה	ABB601/4		538	16.2	228
=	ABG27003	22	264	16.5	231.5
propre	AAB12131		607	9	267
Ω	4		139	0	286.5
Novel human diagno	ABG26897		358	0	9
A human organic an	AAB08824		551	_	295
Human liver-specii	ω		552	1	296.5
A human organic an	82		548	21.1	296.5
ното зар	AAB47272		546	_	307.5
sap	7		538	μ.	307.5
Murine organic an	AAB49401		540	_	
Rat liver anion	AAY51249		535	ω	324.5
Peptide #12329 e	AAM38292		113		344
Peptide #8388 e	AAM21954		113		344
Human bone mar	AAM78066		113		344
Human brain	AAM65378		113		344
Protein #9189 enc	ABB27190		113		344
Peptide #11836	ABB44330		113	*-	(4)
Human osteocias	AAW44196		561		
Rat cerebral orga	AAY92903		536		362.5
Mouse osteoci	AAW44195		537	•	
Novel human secre	AAU33066		128	٠,	w
. Homo	AAB47274		542	.~	386.5
cerebra	AAY92902		542	.~	0
ດ	ABG26899		815		4
	AAB36553		545	-	ω
	AAW88488		551	.~	5
-	AAW88489		563	:~	458.5
	AAB47271		550	.~	58
n organic	AAY44278		550	:~	458.5
ጣ	AAU32379		645	.~	4
n protein			578		588.5
transpor	AAE10336		566	42.0	90
Human organic anio			550		592

## ALIGNMENTS

RESULT AAY52386 HP02000; transmembrane domain; liver; expression; homology; organic cation transporter; drug excretion; antibody; assay reagent; diagnostic marker; primer; probe; antisense; gene therapy; agonist; antagonist; ligand; therapeutic. AAY52386 standard; Protein; 268 AA Homo sapiens Human transmembrane protein HP02000. 09-FEB-2000 (first entry) AAY52386; 04-NOV-1999. W09955862-A2 27-APR-1999; (SAGA ) SAGAMI CHEM RES CENT. (PROT-) PROTEGENE INC. 28-APR-1998; ם 98JP-0119395. 99WO-JP02226.

Human proteins with transmembrane domains, involved in control of cell

N-PSDB; AAZ38316, AAZ38317.

2000-023358/02

Kato S, Kimura T;

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RESULT
AAB47276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                   Modified-site
                                                                                                                                                                        membrane protein; transport; organic anion; splice variant.
                                                                                                                                                                                       Human; organic anion transporter; hOAT; liver; kidney;
                                                Modified-site
                                                                              Modified-site
                                                                                                         Modified-site
                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                       06-AUG-2001
                                                                                                                                                                                                                                                                                      AAB47276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents the protein encoded by human cDNA clone HP02000 which is a 32 kD in size with two putative transmembrane domains. The cDNA was isolated from a human liver cell cDNA library, and from tissue localisation studies has been found to be expressed only in transporter (EMBL Accession No. Y09945) which is involved in drug excretion, and this sequence may have a similar function. The protein may be used to raise specific antibodies, as assay reagents, as diagnostic tissue markers, for the isolation of cognate receptors, ligands and binding proteins, and as biologically active agents. Nucleotides encoding the protein may be used as primers and probes or antisense molecules, and in gene therapy. Cells transformed with these nucleotides may be used to screen for agonists and antagonists which are potentially useful therapeutically.
                                                                                                                                                                                                                            hOAT5
                                                                                                                                                                                                                                                                                                           AAB47276 standard; Protein; 541 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 74-75; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 RICILVFLRKKISRKRHKNDCYTKVTKF 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 VYDQSYFPSTIVTKWDLVCDYQSLKSVVQFLLLTGMLVGGIIGGHVSDRWLVESARWLII 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MAFFEELLSQVGGLGRFQMLHLVFILPSLMLLIPHILLENFAAAIPGHRCWVHMLDNNTGS 60
                                                                                                                                                                                                                                                                                                                                             N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              \verb|tnkldeglkalrkvartngik| naeetlnievvrstm| qeeldaaqtk| ttvcdlfrnpsmrk|
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TNKLDEGLKALRKVARTNGIKNAEETLNIEVVRSTMQEELDAAQTKTTVCDLFRNDSMRK 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vydqsyfpstivtkwdlvcdyqslksvvqfllltgmlvggiigghvsdrwlvesarwlii 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      268 AA;
                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                            /note=
289
                   /note= "PKC phosphorylation site"
526
                                               /note= "PKC phosphorylation site"
345
                                                                                                         Location/Qualifiers
282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 1406; DB 21; 100.0%; Pred. No. 1.2e-143;
"PKC phosphorylation site"
                                                                                     "PKC phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 268;
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ABB11732
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
11-JAN-2002 (first entry)
                                                    ABB11732 standard; peptide; 391 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequences given in AAB47271-76 represent human organic anion transporter (hOAT) polypeptides. hOAT polypeptides are preferentially expressed in the liver and kidneys of humans. OAT's are membrane proteins that facilitate the transport of organic anions across the cell membrane. The mechanism of transport is thought to be a secondary or tertiary active transport involving exchange across the loan tertiary active transport involving exchanges for another organic anion. Identical except at the C-terminal end. hOAT proteins and the DNA encoding them, may be used in the prevention, treatment and diagnosis
                                                                                                                    of diseases associated with inappropriate hOAT expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding human organic anion transporter polypeptides, useful in gene therapy procedures - \,
                                                                                                                                                                          241 lsigqiilgglayvfrdwqtlhvvasvpflgllllqrwlvesarwliitnkldeglkalr 300
                                                                                                                                                                                                                              181 lqlaitdtcaafaptfpvycvlrflagfssmiiisnnslpitewirpnskalvvilssga 240
                                                                                                                                                                                                                                                                                     Claim 2; Fig 6; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-367057/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-JUL-2000; 2000WO-US18980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-JAN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (META-) METABASIS THERAPEUTICS INC.
                                                                                                                                                                                                                                                                                                                                         1 MAFFEELLSQVGGLGRFQMLHLVFILPSLMLLIPHILLENFAAAIPGHRCWVHMLDNNTGS 60
                                                                                    ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                               249;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 541 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88.1%;
69.7%;
                                                                                                                                                                                            -----RWLVESARWLIITNKLDEGLKALR 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1238; DB 22;
Pred. No. 5.2e-125;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Human secreted protein homologue, SEQ ID NO:2102

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CC thrombolytic activities; receptor or ligand activities; or may be completed in oncogenesis, cancer cell proliferation or metastasis.

CC bepending on their biological activities, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include cc cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell cc disorders), chronic inflammatory conditions (e.g., asthma or arthritis), cc proliferative retinopathy, atherosclerosis, coronary heart disease, cc arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal cc vascular growth. Polypeptides involved with tissue regeneration and cc repair (or nucleic acids encoding them) may be used to promote wound cc immunomodulatory activities may be used in the treatment of viral, cc bacterial and fungal infections and ulcers), while those with cc polypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to cantoimmune disease or accidental damage. The polypeptides and nucleotides autoimmune disease or accidental damage. The polypeptides and in drud autoimmune disease or accidental damage. The polypeptides and in drud
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           myeloid cell disorder; lymphoid cell disorder; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiinflammatory; antiarthritic; haemostatic; antiarteriosclerotic; cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial; antifungal; vulnerary; antiulcer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; cytokine; cell proliferation; cell differentiation; growth factor; haematopoiesis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA0825-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell differentiation activities; stem cell growth factor activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis and cancer – \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tang YT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-FEB-2000; 2000US-0496914.
27-APR-2000; 2000US-0560875.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 haematopoiesis regulatory activity; tissue growth activity; immunomodulatory activity; activin- or inhibin-related activities; chemotactic or chemokinetic activities; haemostatic, thrombotic or
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also be used in the diagnosis of the above conditions, and in

antibodies and research use

Isolated polypeptide for treatment of diseases, diagnostics, raising

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SXCC
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AAM24188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    screening techniques. The present sequence represents a novel human polypeptide of the invention.
                                                                                                                                                                                                                                                                              Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse; tomato; monkey; dog; sea urchin; expressed sequence tag; EST; diagnostics; forensic test; gene mapping; genetic disorder; biodiversity; gene therapy; nutrition.
                                                                                                                                                                                                                                                                                                                                          Human EST encoded protein SEQ ID NO: 1713.
                                                                                                                                                                                                                                                                                                                                                                    12-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                 AAM24188 standard; Protein;
                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                           25-JAN-2000; 2000US-0491404.
17-JUL-2000; 2000US-0617746.
03-AUG-2000; 2000US-0631451.
15-SEP-2000; 2000US-0663870.
                                                                                                                                                                                                                                    WO200154477-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAH98847.
                                                                                                     (HYSE-) HYSEQ INC
                                                                                                                                                                                     25-JAN-2001; 2001WO-US02687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GNETGILSEDALLRISIPLDSNLRÞEKCRREVHPQWQLLHLNGTIHSTSEADTEPCVDGW 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27 mafeellsqvggjgrfqmlhlvfilpslmlliphillenfaaaipghrcwvhmldnntgs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lnigqiilgglayvfrdwqtlhvvasvpffvffllsrwlvesarwliitnkldeglkalr 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lqlaitdtcaafaptfpvycvlrflagfssmiiisnnslpitewirpnskalvvilssga 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----RWLVESARWLIITNKLDEGLKALR 192
                                             2001-476164/51.
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                                                                     Drmanac RA,
                                                                                 Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  391 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                 Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88.0%;
                                                                   Du P, Qian
Zhang J, V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                   213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1237; DB 22;
Pred. No. 4.1e-125;
                                                                      Werhman
                                                                                  XB,
                                                                       Wang
nan T;
                                                                                 2
                                                                                   Chen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 391;
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                                                                                   Asundi V;
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Best Local
                                                                                                                                                                                                                Human; transporter and ion channel-10; TRICH-10; cystic fibrosis; mood; gene therapy; amyotrophic lateral sclerosis; amnesia; muscular dystrophy; hypertension; angina; neurological disorder; asthma; bipolar disorder; dementia; depression; Alzheimer's disease; epilepsy; vaccine; arrhythmia; Pick's disease; ischaemic cerebrovascular disease; AIDS; anxiety; stroke; Huntington's disease; mental disorder; cerebral neoplasm; allergy; muscle disorder; cardiomyopathy; cataract; myocarditis; Grave's disease; mental disorder; Schizophrenia; polymyositis; dermatomyositis; diabetes mellitus; immunological disorder; psoriasis; rheumatoid arrhritis; Sjogren's syndrome; systemic lupus erythematosus; sickle cell anaemia; Wilson's disease; infertility; Cushing's disease; scleroderma; pulmonary artery stenosis; nootropic; Addison's disease; mallabsorption syndrome; hypercholesterolaemia; cancer.
                                  WO200146258-A2
                                                                                   Domain
                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                  Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                Human transporter and ion channel-10 (TRICH-10) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE04897 standard; Protein; 553 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 20; Page 1141; 1275pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   198 NGIKNAE 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 MLHLVFILPSLMLLIPHILLENFAAAIPGHRCWVHMLDNNTGSGNETGILSEDALLRISI 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PLDSNLRPEKCRREVHPQWQLLHLNGTIHSTSEADTEPCVDGWVYDQSYEPSTIVTKWDL 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mlhlvfilpslmlliphillenfaaaipghrcwvhmldnntgsgnetgilsedallrisi 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              213 AA;
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                                                                                                               470..493
                                                                                                                                             Location/Qualifiers 204..222
                                                                /label=
                                                                                          /label= Transmembrane_domain
                                                                                                                            abel= Transmembrane_domain
                                                                                 519
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                                                             Transmembrane_domain
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                                                                                                                                                                                                                                                                                                                                        Best
                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                              121
                                                                                                                       Claim 1; Page 122-123; 160pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human transporter and ion channel proteins useful for treating and preventing transport, neurological, muscle and immunological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-418042/44
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02-FEB-2000;
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21-JAN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-FEB-2000;
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                                                                                                                                                                                                                                          l mafqdllghagdlwrfqilqtvflsifavatylhf\mathfrak{m}lenftafipghrcwvhildndtvs 60
                                                                                                                                                                                                                                                                           1 MAFEELLSQVGGLGRFQMLHLVFILPSLMLLIPHILLENFAAAIPGHRCWVHMLDNNTGS
                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                   vydrisfsstivtewdlvcdsqsltsvakfvfmagmmvggilgghlsdrfgrrfvlrwcy 180
                              1 \\quaiv \\gtcaal \\aptfliy \\cslr \\flsgia \\amslit \\ntimlia \\ewathrfqamgitlgmcp
                                                                                                                                                                                                                                                                                                                      160;
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Khan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAD09561.
                                                                                                                                                                                                                                                                                                                                                                                                        553 AA;
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2000US-0176083.
2000US-0177332.
2000US-0178572.
2000US-0179758.
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                                                                                                                                                                                          56.98;
44.78;
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Yue H, Nguyen DB,
                                                                                                                                                                                                                                                                                                                   40;
                                                                                                                                                                                                                                                                                                                                 Score 799.5; DB 22; Pred. No. 1.7e-77;
                                                                                                                                                                                                                                                                                                                   Mismatches
--WLVESARWLIITNKLDEGLKALR
                                                                                                                                                                                                                                                                                                                   49;
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Yao MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yao
                                                                                                                                                                                                                                                                                                                 Indels 109;
                                                                                                                                                                                                                                                                                                                                                 Length 553;
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Gandhi AR;
                                                                                                                                                                                                                                                                                                             Gaps
   192
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membrane protein; transport; organic anion; splice variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      193 KVARTNGIKNAEETLNIEVVRSTMQEELDAAQ-TKTTVCDLFRNPSMRKRICILVFLR 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 sgiafmtlaglafairdwhilqlvvsvpyfvifltsswllesarwliinnkpeeglkelr 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequences given in AABA7271-76 represent human organic anion transporter (hOAT) polypeptides. hOAT polypeptides are preferentially expressed in the liver and kidneys of humans. OAT's are membrane proteins that facilitate the transport of organic anions across the proteins that facilitate the transport of organic anions across the cell membrane. The mechanism of transport is thought to be a secondary cell membrane transport involving exchange of another organic anion. hoAT2A and hOAT2B are thought to be splice variants as they are identical except at the C-terminal end. hOAT proteins and the DNA encoding them, may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate hOAT expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-JUL-2000; 2000WO-US18980.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding human organic anion transporter polypeptides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAC85823
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         useful in gene therapy procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-367057/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Fig 5; 95pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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121 VYDQSYFPSTI-VTKWDLVCDYQSLKSVVQFLLLTGMLVGGIIGGHVSDR------ 169
                                                                                                                         61 GNETGILSEDALLRISIPLDSNLRPEKCRRFVHPQWQLLHLNGTIHSTSEADTEPCVDGW 120
                                                         Local Similarity
                                                                                                                                                                                      1 mafqdilghagdlwrfqilqtvflsifavatylhfmlenftafipghrcwvhildndtvs 60
                                                                                                                                                                                                                                                   1 MAFEELLSQVGGLGRFQMLHLVFILPSLMLLIPHILLENFAAAIPGHRCWVHMLDNNTGS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      554 AA;
                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0143771.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "PKC phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                            54.6%; Score 768; DB 22; Length 554; 43.7%; Pred. No. 4.4e-74;
                                                                                                                                                                                                                                                                                                                                 40; Mismatches
                                                                                                                                                                                                                                                                                                                                           Indels 110; Gaps
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AAM40059
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25-APR-2000; 2000US-0552317.

09-JUL-2000; 2000US-0598042.

19-JUL-2000; 2000US-0620312.

03-AUG-2000; 2000US-0653450.

14-SEP-2000; 2000US-0662191.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; Alzheimer systematics: $\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2
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121 vydrisfsstigdlkwdlvcdsqsltsvakfvfmagmmlggilgvhlsdrfgrsfvlrwc 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human polypeptide SEQ ID NO 3204.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM40059 standard; Protein; 341 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM40059;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               170 -----WLVESARWLIITNKLDEGLKAL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 ylqvalvgtcaalaptfliycsvrflsgiaamsfitntimllaewathrfqamgitlgmc 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-OCT-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200153312-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-DEC-2000; 2000WO-US34263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                leukaemia.
The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, the encoded polypeptides (AAM38642-AAM42213) with nootropic, the inmunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous system fiseases, such as localised neuropathies and central nervous system diseases, such as localised neuropathies and central nervous system disease, amyotrophic Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-SEP-2000; 2000US-0662191.
19-OCT-2000; 2000US-0693036.
29-NOV-2000; 2000US-0727344.
                                                                                                                                                                                                                                                                                                                                                                                   Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries \boldsymbol{\cdot}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-442253/47.
N-PSDB; AAI59215.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                          Example 5; SEQ ID NO 3204; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , Liu C,
Wang Z,
Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Asundi V, Chen R, Ma Y, Wehrman T, Xu C, Xue AJ, Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ren F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wang
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ACCOMMENS OF STREET STR
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AAB19406
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N-PSDB; AAC61892.
                         WPI; 2000-665133/64.
                                                                                           Garcia PD;
                                                                                                                                                                                                                                             09-APR-1999;
                                                                                                                                                    (CHIR ) CHIRON CORP
                                                                                                                                                                                                                20-AUG-1999;
                                                                                                                                                                                                                                                                                         10-APR-2000; 2000WO-US09555.
                                                                                                                                                                                                                                                                                                                                                                                                                          WO200061755-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Secreted protein; platelet disorder; stem cell disorder; osteoporosis; osteoarthiitis; burn; incision; ulcer; periodontal disease; neuropathy; nervous system disease; bone growth; cosmetic plastic surgery;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bone marrow transplantation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino acid sequence of a human secreted protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB19406 standard; Protein; 339 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 kaahrsgmknardtltleilkstmkkeleaagkk 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         193 KVARTNGIKNAEETLNIEVVRSTMQEELDAAOTK 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 sgiafmtlaglafairdwhilqlvvsvpyfvifltsswllesarwliinnkpeeglkelr 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 lqvaivgtcaalaptfliycslrflsgiaamslitntimliaewathrfqamgitlgmcp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       utilisation of the activities such as: Immune system suppression, Activin/Inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 vydrisfsstivtewdlvcdsqsitsvakfvfmagmmvggilgghlsdrfgrrfvlrwcy 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GNETGILSEDALLRISIPLDSNLRPEKCRRFVHPQWQLLHLNGTIHSTSEADTEPCVDGW 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protection; gut regeneration; fibrosis; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                       99US-0150054
                                                                                                                                                                                                                                      99US-0128574
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ~~~~~~WLVESARWLIITNKLDEGLKALR 192
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Novel secreted human proteins useful for stimulating blood cell proteins in patients receiving cancer chemotherapy, treating bone xx marrow transplantation patients and for healing fractured bones . Scalim 14; Page 72; 74pp; English.

CC AAB19393-B19407 represent secreted human proteins. The secreted proteins care useful in assays to determine their biological activities. The cc types which express the proteins. The polynucleotide molecules can be cc used as biomarkers to identify tissues or cell cused as biomarkers for tissues or chromosomes and to elicit immune cc treatment of diseases associated with altered expression of these cc platelet disorders, stem cell disorders, setem cell disorders, osteoporosis or osteoarthritis, con proteins are also useful for prevention or treatment of cc platelet diseases and neuropathies, for healing fractured bones can to induce cartilage and/or bone growth in cosmetic plastic surgery. Cc treatment of lung or liver fibrosis, for stimulating blood cell composition or treatment of the proteins are also useful for gut protection or regeneration, for the generation in patients receiving cancer chemotherapy and for treatment of cof bone marrow transplantation patients.
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Matches
301 kaahrsgmknardtltleilkstmkkeleaaqkkkt 336
                                 193 KVARTNGIKNAEETLNIEVVRSTMQEELDAAOTKTT 228
                                                              241 sgiafmtlaglafairdwhilqlvvsvpyfvifltsswllesarwliinnkpeeglkelr 300
                                                                                                                                  181 lqvaivgtcaalaptfliycllrflsgiaamslitntimliaewathrfqamgitlgmcp
                                                                                                                                                                                                      121 vydrisfssaivtewdlvcdsqsltsvakfvfmagmmvggilgghlsdrfgrrfvlrwcy 180
                                                                                                                                                                                                                            61 GNETGILSEDALLRISIPLDSNLRPEKCRRFVHPQWQLLHLNGTIHSTSEADTEPCVDGW 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                        POCGIT
                                                                                                                                                                                                                                                                                                                                              1 mafqdllghagdlwrfqilqtvflsifavatylhfmlenftafipghrcwvhildndtvs 60
                                                                                                                                                                                                                                                                                                                                                                                1 MAFEELLSQVGGLGRFQMLHLVFILPSLMLLIPHILLENFAAAIPGHRCWVHMLDNNTGS 60
                                                                                                -----WLVESARWLIITNKLDEGLKALR 192
                                                                                                                                                                                                                                                                        dndtgalsqdallristpldsnmrpekcrrfvhpgwgllhlngtfpntsdadmepcvdgw 120
                                                                                                                                                                                                                                                                                                                                                                                                                                       151;
                                                                                                                                                                                                                                                                                                                                                                                                                                              h 54.0%;
Similarity 44.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             33,
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 759; DB 2
Pred. No. 2e-73;
                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB_21; Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                      44; Indels 108;
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                      169
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ARESUSTY 9

AAE10332

ID AAE10332;

XX

AC AAE10332;

XX

DT 10-DEC-2001 (first entry)

XX

Human transporter and ion channel-9 (TRICH-9) protein.

XX

KW neurological disorder; immune disorder; allergy; nootropic; dementia; KW AIDS; Acquired Immune Deficiency Syndrome; amyotrophic lateral sclerosis; Acquired Immune Deficiency Syndrome; amyotrophic lateral sclerosis; KW cystic fibrosis; Alzheimer's disease; depression; epilepsy; scleroderma; KW cystic fibrosis; Alzheimer's disease; depression; epilepsy; scleroderma; treumatoid arthritis; cancer; anaemia; asthma; trauma; haemodialysis; KW gastritis; inflammation.
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25-FEB-2000; 2000US-0184866.
02-MAR-2000; 2000US-0187947.
09-MAR-2000; 2000US-018833.
17-MAR-2000; 2000US-0190230.
17-MAR-2000; 2000US-0192077.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200162923-A2.
                                                                                                                                                                                                    Query Match
Best Local S
                                                                                                                                                                                      Matches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-FEB-2001; 2001WO-US05942.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAR-2000;
                                                                                                                                                                                                                                                                                                          The present sequence is human transporters and ion channels (PRICH-9) protein. The TRICH DNA, protein and their agonist and antagonists are useful in the diagnosis, treatment and prevention of transport disorders (akinesia, amyotrophic lateral sclerosis, cystic transport disorders (akinesia, amyotrophic lateral sclerosis, cystic fibrosis), neurological (Alzheimer's disease, dementia, depression, epilepsy), muscle (e.g. cardiomyopathy, Becker's muscular dystrophy) epilepsy), muscle (e.g. allergies, acquired immunodeficiency immunological disorders (e.g. allergies, acquired immunodeficiency syndrome (AIDS), Crohn's disease, rheumatoid arthritis, scleroderma, syndrome (AIDS), viral, bacterial, parasitic, protozoal and multiple sclerosis), viral, bacterial, parasitic, protozoal and helminthic disorders, cancer, anaemia, asthma, trauma, haemodialysis, helminthic disorders, cancer, anaemia, asthma, trauma, haemodialysis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thirteen human transporters and ion channels (referred to as TRICH-1 to TRICH-13), useful in the diagnosis, treatment and prevention of transport (e.g. akinesia), neurological, muscle or immunological disorders (e.g. allergies) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yue H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-582050/65.
N-PSDB; AAD17476.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 114-115; 131pp; English.
                                                                                                                                                                                                                                                                                                 gastritis and inflammation.
                                                                                                                                                                                                                                                                  Sequence
                               121 VYDQSYFPSTIVTKWDLYCDYQSLKSVVQFLLLTGMLYGGIIGGHVSDR------- 169
                                                            61 asilgsispeallaisippgpnqrphqcrrfrqpqwqlldpnatatswseadtepcvdgw 120
                                                                                             61 GNETGILSEDALLRISIPLDSNLRPEKCRREVHPOWOLLHLNGTIHSTSEADTEPCVDGW 120
                                                                                                                                                         1 MAFEELLSQYGGLGREQMLHLVFILESLMLLIPHILLENFAAAIPGHRCWVHMLDNNTGS 60
                                                                                                                          1 mafselidlvggigrfqviqtmalmvsimwictqsmlenfsaavpshrcwapiidnstaq 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tang YT, Lal P
A, Walia NK, Ga
On M, Greene BD,
   vydrsiftstivakwnivcdshaikpmaqsiylagilvgaaacgpasdrfgrrlvltwsy 180
                                                                                                                                                                                          Similarity 37.8% 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0193500.
                                                                                                                                                                                                                                                                           553 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= Sugar_transporter
204..222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Sugar_transport_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lal P, Policky JL, Nguyen DB, i
K, Gandhi AR, Tribouley CM, Pati
ne BD, Hernandez R, Borowsky ML,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                383
                                                                                                                                                                                                           42.7%; Score 601; DB 22; Length 553; 37.8%; Pred. No. 5.3e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        _sugar_transport_protein
                                                                                                                                                                                                  30; Mismatches
                                                                                                                                                                                                         81; Indels 108; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B, Au-Young J, Patterson C;
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, the encoded polypeptides (AAM38642-AAM42213) with nootropic, are useful communosuppressant and cytostatic activity. The polynucleotides are useful immunosuppressant and cytostatic activity. The polynucleotide or polynucleotide communosuppressant and cytostatic activity, peripheral nervous composition containing a polypeptide or polynucleotide communosuppressed to treat diseases of the peripheral nervous cytostam diseases, such as compositive and central nervous system diseases, such as compositive and central nervous system diseases, such as compositive activity of the activities and containing the activities and systems suppression, commune system suppression, and thrombolytic activity, chamotactic/chemokinetic activity, haemostatic commune systems suppression, and thrombolytic activity, cancer diagnosis and therapy, drug screening, and thrombolytic activity, cancer diagnosis and therapy, drug screening, commune systems suppression, and thrombolytic activity, cancer diagnosis and therapy, drug screening, commune system suppression, and thrombolytic activity, cancer diagnosis and therapy, drug screening, and thrombolytic activity, cancer diagnosis and therapy, drug screening, and the system suppression activity, cancer diagnosis and therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JAN-2000; 2000US-0488725.

25-APR-2000; 2000US-0552317.

29-JUL-2000; 2000US-0598042.

19-JUL-2000; 2000US-0620312.

19-JUL-2000; 2000US-0653450.

14-SEP-2000; 2000US-0662191.

14-CCT-2000; 2000US-0693036.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM41845 standard; Protein; 369 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; peripheral nervous system; neuropathy; central nervous system; cancer; haemostatic; Alzheimer's; parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; thrombolytic; drug screening; arthritis; inflammation; chemokinetic; thrombolytic; drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human polypeptide SEQ ID NO 6776.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAM41845;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 rvaaingkgavqdtitpevllsamreeismgqppaslgtllrmpglrfrtci 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 193 KVARTNGIKNAEETLNIEVVRSTMQEELDAAQTKTTVCDLFRNPSMRKRICI 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200153312-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       leukaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-DEC-2000; 2000WO-US34263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-NOV-2000;
                                                                                                                                                                                                                                                                                                                                Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries \mathring{\ }
                                                                                                                                                                                                                                                                                            Example 2; SEQ ID NO 6776; 10078pp; English.
      C.N.S disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                 2001-442253/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          , Liu C,
Wang Z,
Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                AA161001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0727344
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Asundi V, Chen R, Ma Y, Wehrman T, Xu C, Xue AJ, Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ren F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wang D;
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Specification Note:

The sequence data for this patent did not form part of the printed

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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qγ
Human proteins with hydrophobic domains and the nucleic acids encoding them, useful for preventing diagnosing and treating e.g. cancer,
                                                                 N-PSDB; AAD12607
                                                                                                       Kato S, Kimura T;
                                                                                                                                                                              06-JAN-2000; 2000JP-0000585.
06-JAN-2000; 2000JP-0000588.
11-JAN-2000; 2000JP-0002299.
03-FEB-2000; 2000JP-0026662.
                                                                                                                                             (PROT-) PROTEGENE INC
                                                                                                                                                                         03-MAR-2000;
                                                                                                                                      (SAGA)
                                                                                                                                                                                                                                               28-DEC-2000; 2000WO-JP09359.
                                                                                                                                                                                                                                                                                                          WO200149728-A2.
                                                                                                                                                                                                                                                                                                                                                 Human; hydrophobic domain; gene therapy; nutritional supplement; cell proliferation; immunomodulatory; autoimmune disorder; antimicrobial; multiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes; haematopoiesis; tissue growth activity; Parkinson's disease; oytostatic; Huntington's disease; Alzheimer's disease; chemotactic; chemokinetic; haemostatic; thrombolytic; tumour growth inhibitor; anabolic;
                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human protein having hydrophobic domain, HP03882.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE06612 standard; Protein; 550 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                249 rsgmknardtitleilkstmkkeleaaqkkkpflgerlhmpnickrisllpftk 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          197 TNGIKNAEETLNIEVVRSTMQEELDAAQTKTT-VCDLFRNPSMRKRICILVFLR 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  189 fmtlaglafairdwhilqlvvsvpyfvifltsswilesarwliinnkpeeglkeirkaah 248
                                                                             2001-418355/44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129 ivgtcaalaptfliycslrflsgiaamslitntimliaewathrfqamgitlgmcpsgia 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125 SYFPSTIVTKWDLVCDYQSLKSVVQFLLLTGMLVGGIIGGHVSDR------- 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69 isfsstivtewdivcdsqsitsvakfvfmagmmvggilgghlsdrfgrrfvlrwcylqva 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 GILSEDALLRISIPLDSNLRPEKCRRFVHPQWQLLHLNGTIHSTSEADTEPCVDGWVYDQ 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 galsqdallr1s1pldsnmrpekcrrfvhpgwgllhlngtfpntsdadmepcvdgwvydr 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                SAGAMI CHEM
                                                                                                                                                                   2000JP-0058367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   369 AA;
                                                                                                                                                                                                                                                                                                                                               antiinfertility; antiinflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----WLVESARWLIITNKLDEGLKALRKVAR 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42.3%; Score 594.5; DB 2
41.8%; Pred. No. 1.5e-55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30; Mismatches 32; Indels 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB_22; Length 369;
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AAB69091
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is human protein with hydrophobic domain, CC May be used in the prevention, diagnosis and treatment of diseases CC may be used to produce the polypeptide expression. The polynucleotides CC into a host cell and culturing the cell to express the protein. The polypeptides in diagnostic assays and its complementary sequences may also be used as antigens in the production of antibodies CC polynucleotides and its complementary sequences may also be used as antigens in the production of antibodies and in assays to identify modulators of polypeptide expression and CC activity. The polypeptides and nucleic acids may also be used as antigens in the production of antibodies complements, to modulate cytokine and cell proliferation activity, to middlate cytokine and cell proliferation activity, to creatment of creatment of arminus stimulation or suppression (e.g. for the treatment of creatment of treatment of an arminus and culcimmune disorders such as multiple sclerosis, creatment of provided and insulin-dependent diabetes), to modulate chemotactic and inhibin activity (e.g. for the creatment of treatment of Parkinson's disease, Huntington's disease and Alzheimer's creatment of provided activity, to modulate chemotactic and chemokinetic activity, to controlling condulate haemostatic and thrombolytic activity, to modulate can be controlling and activity, to modulate chemotactic and chemokinetic activity, to modulate can be controlling and activity, to modulate inflammation and to inhibit tumour growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
               Human; organic anion transporter; OAT4; nephrotrophic; kidney disease; abnormal foetal growth.
                                                                        Human organic anion transporter OAT4 protein sequence SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                    24-APR-2001 (first entry)
                                                                                                                                                                                                           AAB69091 standard; Protein; 550 AA
                                                                                                                                                                                      AAB69091;
                                                                                                                                                                                                                                                                                        296 lrkvaringhkea-knitievimssvkeevasakeprsvidlfcvpvirwrscami 350
                                                                                                                                                                                                                                                                                                                             191 LRKVARTINGIKNAEETLNIEVVRSTMQEELDAAQTKTTVCDLFRNPSMRKRICILV 246
                                                                                                                                                                                                                                                                                                                                                                   236 cafsagqaalgglafalrdwrtlqlaasvpffaisliswwlpesarwliikgkpdqaiqe 295
                                                                                                                                                                                                                                                                                                                                                                                                          170 -----WLVESARWLIITNKLDEGLKA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                               176 cclqlavagtstifaptfviycglrfvaafgmagiflssltlmvewtttsrravtmtvvg 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 GWVYDQSYEPSTIVTKWDLVCDYQSLKSVVQFLLLTGMLVGGIIGGHVSDR------ 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 gwvydrsvftstivakwdlvcssqglkplsqsifmsgilvgsfiwgllsyrfgrkpmlsw 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57 gsavstn-mtpkalltisippgpnggphgcrrfrgpgwqlldpnatatswseadtepcvd 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 GSGNETGILSEDALLRISIPLDSNLRPEKCRRFVHPQWQLLHLNGTIHSTSEADTEPCVD 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 42.1%; Score 592; DB 2 Local Similarity 40.2%; Pred. No. 5e-55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MAFEELLSQVGGLGRFQMLH-LVFILPSLMLLIP-HILLENFAAAIPGHRCWVHMLDNNT 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 137-138; 563pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alzheimer's and inflammation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28;
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Best Local
 KW XE XEXX
                                                                                                                                        AAE10336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (NISC-) JAPAN SCI & TECHNOLOGY CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a human placental organic anion transporter, designated OAT4. OAT4 has nephrotrophic activity. The OAT4 protein and encoded gene are useful in studying causes of abnormality, including the application of a variant nucleic acid as a probe to detect the presence of a gene encoding the transporter OAT4, or to identify or the presence of a gene encoding the transporter OAT4, or to identify or quantify such gene, and in developing drugs to prevent or treat various quantify such gene, and abnormal footal growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   placental organic anion transporter gene and encoded polypeptide OAT4, useful in studying causes of abnormality, and in developing drugs to prevent or treat various kidney diseases and abnormal fetal growth -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2; Page 26-28; 32pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                kidney diseases and abnormal foetal growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                              119
                                                                                                                                                                                                                                                                                                         176 cclqlavagtstifaptfviycglrfvaafgmagiflssltlmvewtttsrravtmtvvg 235
Human; transporter and ion channel; TRICH-13; therapy; akinesia; neurological disorder; immune disorder; allergy; nootropic; dementia;
                                                                                                 AAE10336;
                                                                                                                             AAE10336 standard;
                                                                                                                                                                                                                          191 LRKVARTNGIKNAEETLNIEVVRSTMGEELDAAGTKTTVCDLFRNESMRKRICILV 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                     59
                                       Human transporter and ion channel-13 (TRICH-13) protein
                                                                                                                                                                                               57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MAFEEULSOVGGLGREOMLH-LVFILPSLMLLIP-HILLENFAAAIPGHRCWVHMLDNNT 58
                                                                         10-DEC-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001-138139/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gsavstn-mtpkalltisippgpnggphgcrrfrgpqwqlldpnatatswseadtepcvd 115
                                                                                                                                                                                                                                                                                                                                                                gwvydrsvftstivakwdivcssqglkplsqsifmsgilvgsfiwgllsyrfgrkpmlsw 175
                                                                                                                                                                                                                                                                                                                                                                                            GWYYDQSYEPSTIVTKWDLVCDYQSLKSVVQFLLLTGMLVGGIIGGHVSDR------ 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSGNETGILSEDALLRISIPLDSNLRPEKCRREVHPQWQLLHLNGTIHSTSEADTEPCVD 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      143; Conservative
                                                                                                                                                                                                                                                      {\tt cafsagqaalgglafalrdwrtlqlaasvpffaisliswwlpesarwliikgkpdqalqe}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAF32614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                h 42.18;
Similarity 40.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sekine T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          550 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000WO-JP03878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99JP-0187244.
                                                                                                                                   Protein; 566 AA
                                                                                                                                                                                                                                                                                      -----WLVESARWLIITNKLDEGLKA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 592; DB 2
Pred. No. 5e-55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22; Length 550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69;
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                                                                                                                                                                                                                                                                                                                                                             .____ 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gastritis; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200162923-A2.
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                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-FEB-2000; 2000US-0184866,
02-MAR-2000; 2000US-0187947,
09-MAR-2000; 2000US-0188333,
01-MAR-2000; 2000US-0190230,
24-MAR-2000; 2000US-0192077,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-FEB-2001; 2001WO-US05942
                                                                                                                                                                                                                                                                                                                  The present sequence is human transporters and ion channels (TRICH-13) protein. The TRICH DNA, protein and their agonist and transporters are useful in the diagnosis, treatment and prevention of antagonists are useful in the diagnosis, treatment and prevention of transport disorders (akinesia, amyotrophic lateral sclerosis, cystic transport disorders (akinesia, amyotrophic lateral sclerosis, cystic transport disorders (e.g. cardiomyopathy, Becker's muscular dystrophy) or immunological disorders (e.g. allergies, acquired immunodeficiency syndrome (AIDS), crohn's disease, rheumatoid arthritis, scleroderma, syndrome (AIDS), crohn's disease, rheumatoid arthritis, protozoal and multiple sclerosis), viral, bacterial, parasitic, protozoal and helminthic disorders, cancer, anaemia, asthma, trauma, haemodialysis, helminthic disorders, cancer, anaemia, asthma, trauma, haemodialysis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thirteen human transporters and ion channels (referred to as TRICH-1 to TRICH-13), useful in the diagnosis, treatment and prevention of transport (e.g. akinesia), neurological, muscle or immunological disorders (e.g. allergies)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yue H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thornton M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 119-120; 131pp; English.
                                                                                                                                                                                                                                                                                                         gastritis and inflammation.
                                                                                                                                                                                                                                                                         Sequence
119 GWYYDQSYFPSTIVTKWDLVCDYQSLKSVVQFLLLTGMLVGGIIGGHVSDR------ 169
                                                                                                                                                                                                             Local
                                                                                                59
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                                                                  57
                                                                                                                                                            1 MAFEELLSQVGGLGREQMLH-LVFILPSLMLLIP-HILLENFAAAIPGHRCWVHMLDNNT 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001-582050/65.
                                                                                                                            mafskileqaggyglfqtiqvltfilpclm--ipsqmllenfsaaipghrcwthmldn-- 56
                                                                                             GSGNETGILSEDALLRISIPLDSNLRPEKCRRFVHPQWOLLHLNGTIHSTSEADTEPCVD 118
                                                             gsavstn-mtpkalltisippgpnggphqcrrfrqpqwqlldpnatatswseadtepcvd 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tang YT, L
                                                                                                                                                                                                 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAD17480
                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0187947.
2000US-0188333.
2000US-0190230.
2000US-0192077.
2000US-0193500.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Greene BD,
                                                                                                                                                                                                                                                                                566 AA;
                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers 103..543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= Transmembrane_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label=_Sugar_transporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lal P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gandhi AR, Tribo
BD, Hernandez R,
                                                                                                                                                                                                                   42.0%; Score 590.5; DB 2
39.0%; Pred. No. 7.6e-55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Policky JL,
                                                                                                                                                                                                          32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         y JL, Nguyen DB,
Tribouley CM, P
                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Borowsky ML,
                                                                                                                                                                                                                                           DB 22; Length 566;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                patterson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Au-Young J,
atterson C;
                                                                                                                                                                                                                 Indels 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sanjanwala MS;
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The present sequence is human protein with hydrophobic domain, Hp03613.
The polynucleotide and polypeptide of the invention may be used in the prevention, diagnosis and treatment of diseases associated with the control of interest of the polypeptide with the control of the polynucleotides may be used to produce the polypeptide, by inserting the nucleic acids into a host control of the polynucleotides may be used and its complementary sequences may also be used as DNA probes in the polynucleotides and the used in gene therapy. The polypeptides may control of the didentify modulators of polypeptide expression and activity. The polypeptides and nucleic acids may be used as nutritional supplements, immune stimulation or suppression (e.g. for the treatment of microbial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE06571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Qγ
                                                                                                                                                                                                                                                Claim 1; Page 59-60; 563pp; English.
                                                                                                                                                                                                                                                                                   Alzheimer's and inflammation
                                                                                                                                                                                                                                                                                Human proteins with hydrophobic domains and the nucleic acids encoding them, useful for preventing diagnosing and treating e.g. cancer,
                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAD12566.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-JAN-2000; 2000JP-0000585.
06-JAN-2000; 2000JP-0000588.
11-JAN-2000; 2000JP-0002299.
03-FEB-2000; 2000JP-0026862.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-DEC-2000; 2000WO-JP09359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cell proliferation; immunomodulatory; autoimmune disorder; antimicrobial; multiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes; haematopoiesis; tissue growth activity; Parkinson's disease; cytostatic; Huntington's disease; Alzheimer's disease; chemotactic; chemokinetic; haemostatic; thrombolytic; tumour growth inhibitor; anabolic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W0200149728-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            contraceptive; antiinfertility; antiinflammatory.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human protein having hydrophobic domain, HP03613.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE06571 standard; Protein; 578 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 191 LRKVARTNGIKNAEETLNIEVVRSTMQEELDAAQTKTTVCDLFRNPSMRKRICILVFLR 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              296 lrkvaringhkeetecvylkvlmssvkeevasakeprsvldlfcvpvlrwrscamlvvk 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            236 cafsagqaalgglafalrdwrtlqlaasvpffaisliswwlpesarwliikgkpdqalqe 295
                                                                                                                                                                                                                                                                                                                                                                      2001-418355/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------WLVESARWLIITNKLDEGLKA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cclqlavagtstifaptfviycglrfvaafgmagiflssltlmvewtttsrravtmtvvg 235
                                                                                                                                                                                                                                                                                                                                                                                                                                 SAGAMI CHEM RES CENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEGENE INC
                                                                                                                                                                                                                                                                                                                                                                                                     Kimura T;
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       Tang YT,
                                     (HYSE-) HYSEQ INC.
                                                                   26-JAN-2001; 2001US-0770160
                                                                                                                        16-APR-2001; 2001WO-US08656.
                                                                                            18-APR-2000;
                                                                                                                                                                    25-OCT-2001.
                                                                                                                                                                                                       W0200179449-A2.
                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                 Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopoiesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemi;
                                                                                                                                                                                                                                                                                                                                      Novel human secreted protein #2870.
                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU32379 standard; Protein; 645 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 133;
                                                                                                                                                                                                                                                                                                                                                                             18-DEC-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361 slgtllrmpglrfrtci 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               228 TVCDLFRNPSMRKRICI 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 swwlaesarwllttgrldwglqelwrvaaingkgavqdtltpevllsamreelsmgqppa 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               170 --WLVESARWLIITNKLDEGLKALRKVARTNGIKNAEETLNIEVVRSTMOEELDAAOTKT 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 lgllavmewtaararplvmtlnslgfsfghgltaavaygvrdwtllqlvvsvpfflcfly 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181\ lg{\tt mavmgtaaafapafpvyclfrfllafavagv{\tt mmntgtlrrsltwrhagglhagsraep}}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       infections and autoimmune disorders such as multiple sclerosis, rheumatoid arthritis and insulin-dependent diabetes), to modulate haematopoiesis, to modulate tissue growth activity (e.g. for the treatment of Parkinson's disease, Huntington's disease and Alzheimer's disease), to modulate activin and inhibin activity (e.g. for controlling modulate haemostatic and thrombolytic activity, to modulate receptor ligand activity, to modulate inflammation and to inhibit tumour growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 VYDQSYFPSTIVTKWDLYCDYQSLKSVVQFLLLTGMLVGGIIGGHVSDR------ 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 asilgslspeallaisippgpnqrphqcrrfrqpqwqlldpnatatswseadtepcvdgw 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GNETGILSEDALLRISIPLDSNLRPEKCRRFVHPQWQLLHLNGTIHSTSEADTEPCVDGW 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 mafselidlyggigrfqviqtmalmvsimwictqsmlenfsaavpshrcwaplldnstag 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MAFEELLSQVGGLGREQMLHLVFILPSLMLLIPHILLENFAAAIPGHRCWVHMLDNNTGS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vydrsiftstivakwnlvcdshalkpmaqsiylagilvgaaacgpasdrfgrrlvltwsy 180
 Liu C,
                                                                                         2000US-0552929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     578 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41.9%; Score 588.5; DB 2
35.3%; Pred. No. 1.3e-54;
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DR WPI; 2001-611725/70.

XX Nucleic acids encoding a range of human polypeptides, useful in genetic PT vaccination, testing and therapy -

XX Claim 20; Page 597; 765pp; English.

XX The invention relates to novel human secreted polypeptides. The CC polypeptides and antibodies to the polypeptides are useful for CC determining the presence of or predisposition to a disease associated CC with altered levels of polypeptide. The polypeptides are also useful for CC identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent CC physiological interactions of the polypeptides. Vectors comprising CC the nucleic acids encoding the polypeptides and cells genetically CC engineered to express them are also useful for producing the proteins. They may be used to therapy, and can be useful in genetic vaccination, testing and concease stem cell proliferation; to regulate haematopoissis; and in CC increase stem cell proliferation; to regulate haematopoissis; and in treatment of leukaemias. AAA/29510-AAA/33/34 represent the amino acid sequences of novel human secreted proteins of the invention.

XX Sequence 645 AA;

Query Match Basicarvative 31. Mismatches 63; Indels 218; Gaps 6;

Marches 126. Conservative 31; Mismatches 63; Indels 218; Gaps 6;
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рь δÃ 밁 VΩ Ωy В δÃ 밁 δÃ 밁 Š 밁 Ş В Best Local Similarity Matches 126; Conserv 170 116 lkplsqsifmsgilvgsfiwgllsyrfgrkpmlswcclqlavagtstifaptfviycglr 175 236 aasvpffaisliswwlpesarwliikgkpdqalqelrkvaringhkeaknltietppppp 295 170 176 fvaafgmagiflssltlmvewtttsrravtmtvvgcafsagqaalgglafalrdwrtlql 235 144 LKSVVQFLLLTGMLVGGIIGGHVSDR----- 169 232 LFRNPSMRKRICILVFLR 249 356 insthtvtsithhlhhvarthlmgvldvsgetecvylkvlmssvkeevasakeprsvld 415 296 pipipsptapplstptitftaitpsppappipsltpqppslqnisttfttivtignstii 355 56 gphqcrrfrqpqwqlldpnatatswseadtepcvdgwvydrsvftstivakwdlvcssqg 115 84 RPEKCRREVHPQWQLLHLNGTIHSTSEADTEPCVDGWVYDQSYFPSTIVTKWDLVCDYQS 143 25 LPSIMILIP-HILLENFAAAIPGHRCWVHMLDNNTGSGNETGILSEDALLRISIPLDSNL 83 1 lpclm--ipsqmllenfsaaipghrcwthmldn--gsavstn-mtpkalltisippgpng 55 ------WLVESARWLIITNKLDEGLKALRKVARTNGIKNAE----lfcvpvlrwrscamlvvk 433 33.6%; Score 472; DB 22; Length 645; illarity 28.8%; Pred. No. 6.3e-42; Conservative 31; Mismatches 63; Indels 218; Gaps :: :: = <del>..</del> ----ETLNIEVVRSTMQEELDAAQTKTTVCD 231 204 204 6;

Search completed: July 1, 2002, 11:39:06 Job time: 372 sec

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Title:
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     protein search, using sw model
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1: /ggn2_6/ptodata/2,
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3: /cgn2_6/ptodata/2,
4: /ggn2_6/ptodata/2,
5: /ggn2_6/ptodata/2,
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US-09-040-444-3
US-08-501-572-3
US-09-040-444-2
US-08-501-572-2
US-08-964-127-2
US-08-964-127-4
US-09-96-692-2
US-08-96-92-386-7
US-09-96-692-7
US-09-99-386-7
US-09-99-386-7
US-09-99-38-7
US-09-99-549-5
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Qy 1 MAFEELLSQVGGIGREQMIHIVFILPSIMILIPHILLENPAAAIPCHRCW 1   1   1   1   1   1   1   1   1   1	Query Match 26.1%; Score 367.5; DB 2; Best Local Similarity 24.6%; Pred. No. 1.2e-33; Matches 88; Conservative 45; Mismatches 74;	US-08-647-397-2 US-08-647-397-2 US-08-647-397-2 Sequence 2, Application US/08647397 Fatent No. 5972702 Fatent No. 5972702 Fatent No. 5972702 GENERAL INFORMATION: APPLICANT: Beier, David R. RODRESSE: GOTEROCLAST TRANSPORTER NUMBER OF SEQUENCES: 6 CORRESPONDENCE ADDRESS: APPLICATION CORPACTION AVENUE COMPUTER EADABLE FORM: COMPUTER EADABLE FORM: COMPUTER: INP C COMPATIBLE COMPANIES: PLOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION UNMBER: US/08/647,397 FILING DATE: CURSIFICATION UNMBER: B0801/7048 RESERENCE/DOCKET NUMBER: B0801/7048 RESERENCE/DOCKET NUMBER: B0801/7048 RELECOMMUNICATION INFORMATION: TELEPHONE: 617-720-3500 TELEPHONE: 617-720-3500 TELEPHONE: 617-720-3500 TELEPHONE: 617-720-3500 TELEPHONE: 617-720-3500 TELEPHONE: 617-720-3500 TELEPHONE: 617-720-2441 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LEGGTH: 537 amino acids TYPE: protein NUS-08-647-397-2	28 79 5.6 393 3 US-09-187-050-16 29 79 5.6 393 3 US-09-187-050-20 30 79 5.6 393 3 US-09-187-050-20 31 79 5.6 393 3 US-09-187-050-24 32 79 5.6 393 3 US-09-187-050-24 33 79 5.6 393 3 US-09-187-050-26 34 79 5.6 393 3 US-09-187-050-27 34 79 5.6 393 3 US-09-187-050-28 35 79 5.6 393 3 US-09-187-050-29 36 79 5.6 393 3 US-09-187-050-30 37 79 5.6 393 3 US-09-187-050-30 38 79 5.6 393 3 US-09-187-050-30 39 79 5.6 393 3 US-09-187-050-31 40 79 5.6 393 3 US-09-187-050-31 41 77 5.6 393 3 US-09-187-050-34 42 76.5 5.4 1642 1 US-09-176-320-8 43 76.5 5.4 1642 1 US-08-447-411-45 45 76.5 5.4 1642 2 US-08-662-227-2 45 76.5 5.4 1642 4 US-09-017-947-2
IPGHRCW 50 IPDHHCRPPPNASLEPW 60	th 537; ls 151; Ga		Sequence 16, Appl Sequence 20, Appl Sequence 22, Appl Sequence 24, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 29, Appl Sequence 30, Appl Sequence 31, Appl Sequence 32, Appl Sequence 32, Appl Sequence 33, Appl Sequence 34, Appl Sequence 37, Appl Sequence 37, Appl Sequence 38, Appl Sequence 37, Appl Sequence 38, Appl Sequence 45, Appl Sequence 27, Appli Sequence 27, Appli Sequence 27, Appli Sequence 27, Appli

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MOLECULE TYPE: peptide	76-0
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TELEPHONE: (202)408-4000 TELEFAX: (202)408-4400	٠. ٠.
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NAME: TOOhey, Kimberlin M REGISTRATION NUMBER: 35,391	
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STREET: 1300 I Street, N.W., Suite 700	· · · ·
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Dirk Valenti	
ANT: Koepsell, E	
Patent No. 6063623	
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; MOLECULE TYPE: peptide US-09-040-444-1
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Patent No. 6063766
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                          TELEFAX: (202)408-4400
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 556 amino acids
                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)408-4000
                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Koepsell, Hermann
APPLICANT: Grundeman, Dirk
APPLICANT: Grundeman, Dirk
APPLICANT: Gorboulev, Valentin
TITLE OF INVENTION: Transport protein Which Effects The
TITLE OF INVENTION: Transport Of Cattonic Xenobiotics and\or Pharmaceuticals,
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
Match 12.1%; Score 169.5; DB 3; Length 556; Local Similarity 20.5%; Pred. No. 7.8e-11; Les 77; Conservative 47; Mismatches 95; Indels 157; Gaps
                                                                                                                                                                                                                                                                                                                                                       NAME: O'Connor, Steven P
REGISTRATION NUMBER: 41,225
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/0. FILING DATE: March 18, 1998
                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE:
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CITY: Washington
STATE: D.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             175 ARWLIITNKLDEGLKALRKVARTNG-IKNAEETLNIEVVRSTMQEELDAAQTKT-TVCDL 232
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SYSTEM: PC-DOS/MS-DOS
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US-08-501-572-3
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Patent NO. 6063623
GENERAL INFORMATION:
APPLICANT: Koepsell, Hermann
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US-08-501-572-3
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TITLE OF INVENTION:
TITLE OF INVENTION:
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CORRESPONDENCE ADDRESS:
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                                                                                                              TELEFAX: (202)408-4400 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: TOODBY, Kimberlin M
REGISTRATION NUMBER: 35,391
REFERENCE/DOCKET NUMBER: 02
                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                  MOLECULE TYPE: peptide
                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM:
                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                    TELEPHONE:
                                     TOPOLOGY:
                                                    STRANDEDNESS
                                                                                   LENGTH:
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1300 I Street, N.W., Suite 700
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Gorboulev, Valentin
                                                                      amino acid
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                                                                                    555 amino acids
                                                                                                                                     (202)408-4400
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IBM PC compatible
;YSTEM: PC-DOS/MS-DOS
                                           linear
                                                                                                                                                     (202)408-4000
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US-09-040-444-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                              REFERENCE/DOCKET NUMBER: 2481
TELECOMMUNICATION INFORMATION: 2021408-4400
TELEFAX: 2021408-4400
INFORMATION FOR SEQ ID NO: 3:
INFORMATION FOR SEQ ID NO: 3:
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APPLICANT: Grundeman, Dirk
APPLICANT: Grundeman, Dirk
APPLICANT: Gorboulev, Valentin
TITLE OF INVENTION: Transport of Cationic Xenobiotics and or Pharmaceuticals,
TITLE OF INVENTION: DNA Sequences Encoding It And Their Use.
TITLE OF INVENTION: DNA Sequences Encoding It And Their Use.
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                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: O'CONDOY, Steven P
                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC COMPATIBLE PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OFTWARE: Patentin Release #1.0, Version #1.30 SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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                                                      MOLECULE TYPE: peptide
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                                                                        STRANDEDNESS:
TOPOLOGY: li
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1300 I Street, N.W., Suite 700
                                                                                                          amino acid
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US-09-040-444-3
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
                                                                              CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Toohey, Kimberlin M
REGISTRATION NUMBER 35,391
TELECHMUNICATION INFORMATION:
TELECHNONE: (202)408-4000
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             STRANDEDNESS:
      TOPOLOGY:
                                 TYPE:
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                       amino acid
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1300 I Street, N.W., Suite 700
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ATTORNEY/AGENT INFORMATION:
NAME: O'CONDOY, Steven P
REGISTRATION NUMBER: 41,225
REFERENCE/DOCKET NUMBER: 2481.1453-01
TELEPHONE: (202)408-4000
TELEPAX: (202)408-4000
INFORMATION FOR SEQ ID NO: 2:
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                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                         CLASSIFICATION
                                                                                                                                 APPLICATION NUMBER: FILING DATE: March
                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                        ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner, L.L.P.
                                                                                                                                                                                                                                                                           STATE: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114 SHLPLGPCQDGWYYDTP--GSSIVTEFNLVCADSWKLDLFQSCLNAGFFFGSLGVGYFAD 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109 SEADTEPCVDGWYYDQSYFPSTIYTKWDLVCDYQSLKSVVQFLLLTGMLVGGIIGGHVSD 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 -----WSPAEELNYTVP---GLGPAGEAFLGQCRRY-EVDWNQSALSCVDPLASLATNR 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GNETGILSEDALLRISIPLDSNIRPE-----KCRREVHPOWQLLHLN-----GTIHST 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 DDILEQVGESGWFOKOAFLILCLLSAAFAPICVGIVFLGFTPDHHCOSPGVAELSORCG- 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 EELLSQVGGLGRFQMLHLVFILESLMLLIPHILLENFAAAIPGHRC---WVHMLDNNTGS 60
                                                                                                                                                                                                                                           20005-3315
                                                                                                                                                                                                                                                                                                                                                                                                                                                        2, Application US/09040444
5. 6063766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               s 75; Conserv
                                                                                                                                                                                                                                                                                                                  Grundeman, Dirk
Gorboulev, Valentin
WENTION: Transport protein Which Effects The
WENTION: Transport Of Cationic Xenobiotics and or Pharmaceuticals,
On Sequences Encoding It And Their Use.
                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                 Koepsell, Hermann
                                                                                                                                  March 18, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                          US/09/040,444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.4%; Score 146; DB 3; Length 553; 20.4%; Pred. No. 3.9e-08; ative 34; Mismatches 117; Indels 142; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11;
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; MOLECULE TYPE: peptide US-09-040-444-2
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US-08-964-127-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08964127
Patent No. 6277565
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                 OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Grandearl, Andrew David John
TITLE OF INVENTION: NOVEL GENES ENCODING TRANSPORTER-LIKE
TITLE OF INVENTION: MOLECULES
                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                         FILING DATE: 06-NOV-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     292 QKRNTEAIKIMDHIAQKNG-KLPPADLKMLSLEEDVTEKL----SPSFADLFRTPRLRK 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  170 ------WLV-ESARWLII 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         172 RFGRKLCLLGTVLVNAVSGVLMAFSPNYMSMLLFRLLQGLVSKGNWMAGYTLITEFVGSG 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114 SHLPLGPCQDGWYYDTP--GSSIVTEFNLVCADSWKLDLFQSCLNAGFFFGSLGVGYFAD 171
                                        ATTORNEY/AGENT INFORMATION: NAME: Crews, Ph.D., L. I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 RICILVEL 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 THKLDEGLKALRKVARTNGIKNAEETLNIEVVRSTMQEELDAAQTKTTVCDLFRNPSMRK 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        232 SRRTVAIMYQMAFTVGLVALTGLAYALPHWRWLQLAVSLPTFLFLLYYWCVPESPRWLLS 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109 SEADTEPCVDGWVYDQSYFPSTIVTKWDLVCDYQSLKSVVQFLLLTGMLVGGIIGGHVSD 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       346 RTFILMYL 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 -----WSPAEELNYTVP----GLGPAGEAFLGQCRRY-EVDWNQSALSCVDPLASLATNR 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GNETGILSEDALLRISIPLDSNLRPE-----KCRRFVHPQWQLLHLN------GTIHST 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
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                                                                                                                                                                                                                           COMPUTER: IBM Com
OPERATING SYSTEM:
                                                                                FILING DATE:
                                                                                                                                               APPLICATION NUMBER: US/08/964,127 FILING DATE: 06-NOV-1997
                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                      CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
               NAME: Crews, Ph.D., L. Lee
REGISTRATION NUMBER: P-43,
REFERENCE/DOCKET NUMBER:
                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DDILEQVGESGWFQKQAFLILCLLSAAFAPICVGIVFLGFTPDHHCQSPGVAELSQRCG- 63
                                                                                                                                                                                                                                                                                                                       02110-2804
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                                                                                                                                                                                                                                                                                                                                                                                                          225 Franklin Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34; Mismatches 117; Indels 142; Gaps
                                          Lee
  07334/038001
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; MOLECULE TYPE: protein ; FRAGMENT TYPE: internal US-08-964-127-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 2, Application US/09496692 ; Patent No. 6313271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Grandearl, Andrew David John
TITLE OF INVENTION: NOVEL GENES ENCODING TRANSPORTER-LIKE
TITLE OF INVENTION: MOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: U.T. 200154
                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS: address: Fish & Richardson P.C
                                                                                                                                                                 OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                 APPLICATION NUMBER: 08/964,127
FILING DATE: 06-NOV-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 228 TYCDL-----FRNPSMRKRICILVFLRKKISRKRHKNDCYTKV 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            233 PGLFLESARWLIVKRQIEEAQSVLRILAERN--RPHGQMLG-----EEAQEALQDLE 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 171 ---LVESARWLIITNKLDEGLKALRKVARTNGIKNAEETLNIEVVRSTMQEELDAAOTKT 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         173 YLMRLELCDPTQRLRVALAGELVGVGGHFLFLGLALVSKDWRFLQRMITAPCILFLFYGW 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   153 -----LTGMLVGGI---- 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            283 NTCPLPATSSFSFASLLNYRN--IWKNLLILGFTNFIAHAIRH---CYQPV 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 01//542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 HYGAFPPNASGW-EQPPNASGVSVASAALAASAASRVATSTDPS-----CSGFAPP---- 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39 NFAAAIPGHRCWVHMLDNNTGSGNETGILSEDALLRISIPLDSNLRPEKCRRFVHPQWQL 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99 LHLNGTIHSTSEADTEPCVDGWVYD-QSYFPSTIVTKWDLVCD--YQSLKSVVQFLL--- 152
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                                                                                                                                                                                                                                                                                                                                      CITY:
STATE:
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                                                                                                                                                                                                                                                                                              ZIP:
                                                                                                                       APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Fish a ...
STREET: 225 Franklin Street
NAME: Crews, Ph.D., L. Lee REGISTRATION NUMBER: P-43,567
                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGYLFLGYPADRFGRRGIVLLTLGLVGPCGVGGAAAGSSTGVMALRFLLGFLLAGVDLGV 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----DFNHCLKDWDYNGLPVLTTNAIGQWDLVCDLGWQVILEQILFILGFA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    h 7.4%; Score 104; DB 4; Length 520;
Similarity 18.2%; Pred. No. 0.0025;
64; Conservative 33; Mismatches 92; Indels 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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US-08-928-692-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 12, APF1-
Sequence 10, S958727
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TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
APPLICANT:
                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,692
FILING DATE: 12-SEPT-1997
                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS: No. 59587270 No. 5958727d1sk of No. 5958727th America, Inc.
                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hansen, Kim
TITLE OF INVENTION: Methods for MC
TITLE OF INVENTION: a POlypeptide
                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 07334/038001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           283 NTCPLPATSSFSFASLLNYRN--IWKNLLILGFTNFIAHAIRH---CYQPV 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        233 PGLFLESARWLIVKRQIEEAQSVLRILAERN--RPHGQMLG-----EEAQEALQDLE 282
                       CLASSIFICATION:
                                                                                                  COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Wil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 228 TYCDL-----FRNPSMRKRICILVFLRKKISRKRHKNDCYTKV 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              171 ---LVESARWLIITNKLDEGLKALRKVARTNGIKNAEETLNIEVVRSTMQEELDAAQTKT 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173 YLMRLELCDPTQRLRVALAGELVGVGGHFLFLGLALVSKDWRFLQRMITAPCILFLFYGW 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         153 -----LTGMLVGGI---- 161
                                                                                                                                                                                                       ZIP: 10174
                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                           CITY: New York
                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 -----DENHCLKDWDYNGLPVLTTNAIGQWDLVCDLGWQVILEQILFILGFA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99 LHLNGTIHSTSEADTEPCVDGWVYD-QSYFPSTIVTKWDLVCD--YQSLKSVVQFLL--- 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 HYGAFPPNASGW-EQPPNASGVSVASAALAASAASRVATSTDPS-----CSGFAPP---- 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39 NFAAAIPGHRCWVHMLDNNTGSGNETGILSEDALLRISIPLDSNLRPEKCRRFVHPQWQL 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/08928692
                                                                                                                                                                                                                                                                              405 Lexington Avenue
                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                              Brody, Howard
Yaver, Deborah S.
Lamsa, Michael
                                                                                                FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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18.2%; Pred. No. 0.0025; Indels 162; Gaps
ative 33; Mismatches 92; Indels 162; Gaps
                                                                                                                                                                                                                                                                                                                                                                  Methods for Modifying the Production of
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US-08-964-127-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear; MOLECULE TYPE: No. 5958727e US-08-928-692-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/08964127 Patent No. 6277565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 7.1%; Score 100; DB 2; Best Local Similarity 27.6%; Pred. No. 0.0072; Matches 35; Conservative 22; Mismatches 3
                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/964,127
FILING DATE: 06-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                     REFERENCE/DOCKET NUMBER: 07334/038001 TELECOMMUNICATION INFORMATION: TELEPHONE: 617/542-5070
                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                          FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Crews, Ph.D., L. Lee
REGISTRATION NUMBER: P-43.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Grandearl, Andrew David John TITLE OF INVENTION: NOVEL GENES ENCODING TITLE OF INVENTION: MOLECULES
                                                                                TELLETAX: OI.,
TELEFAX: 200154
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            LENGTH: 286 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  304 ILVALML 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    242 ICILVFL 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  250 LDEEVKAKQSLKRLRGYDDVTKDIN-----EMRKEREEASSEQKVSIIQLFTNSSYRQP 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      184 LDEGLKALRKVARTNGIKNAEETLNIEVVRSTMQEELDAA--QTKTTVCDLFRNPSMRKR 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              193 QLAIVTGILISQIIGLEFILGNY-DLWHILLGLSGVRAILQSLLLFFCPESPRYLYI--K 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  149 QFLLLTGMLVGGIIG-----GHVSDRWLV------ESARWLIITNK 183
TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 02110-2804
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REGISTRATION NUMBER: 33
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
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                                                                                                                617/542-8906
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TOPOLOGY: linear

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US-08-964-127-4
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Matches 54; Conservative
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FRAGMENT TYPE:
                                                        TELEX: 200154
[NFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Grandearl, Andrew I TITLE OF INVENTION: NOVEL GENE TITLE OF INVENTION: MOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162 ------ 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113 SGYLFLGYPADRFGRRGIVLLTLGLYGPCGYGGAAAGSSTGVMALRFLLGFLLAGVDLGV 172
                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            173 YLMRLELCDPTQRLRVALAGELVGVGGHFLFLGLALVSKDWRFLQRMITAPCILFLFYGW 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                153 -----LTGMLVGGI---- 161
                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Crews, Ph.D. 1. 1.
                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                233 PGLFLESARWLIVKROIEEAQSVLRILAERNRPHGQMLGEEA------QEALQDLE 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      171 ---LVESARWLIITNKLDEGLKALRKVA---RTNGIKNAEETLNIEVVRSTMQEELDAAQ 224
                                                                                                                 TELECOMMUNICATION INFORMATION: 517/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         283 SST 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 225 TKT 227
                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 HYGAFPPNASGW-EQPPNASGVSVASAALAASAASRVATSTDPS-----CSGFAPP---- 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39 NFAAAIPGHRCWVHMLDNNTGSGNETGILSEDALLRISIPLDSNLRPEKCRRFVHPQWQL 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 -----DFNHCLKDWDYNGLPVLTTNAIGQWDLVCDLGWQVILEQILFILGFA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99 LHLNGTIHSTSEADTEPCVDGWVYD-QSYFPSTIVTKWDLVCD--YQSLKSVVQFLL--- 152
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                                                                              TELEPHONE: 01//-
TELEPHONE: 01//-
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                                                                                                                                                       NAME: Crews, Ph.D., L. Lee
REGISTRATION NUMBER: P-43,567
REFERENCE/DOCKET NUMBER: 07334/038001
                                                                                                                                                                                                                                                                                              FILING DATE
                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02110-2804
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                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 06-NOV
                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                LENGTH:
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amino acid
                  286 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                               IBM Compatible
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internal
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17.8%; Pred. No. 0.0043;
rative 29; Mismatches 73; Indels 147; Gaps
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; MOLECULE TYPE:
; FRAGMENT TYPE:
US-09-496-692-4
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US-08-989-386-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: HUMAN ISOMERASE HOMOLOGS NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
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                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            171 ---LVESARWLIITNKLDEGLKALRKVA---RTNGIKNAEETLNIEVVRSTMQEELDAAQ 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173 YLMRLELCDPTQRLRVALAGELVGVGGHFLFLGLALVSKDWRFLQRMITAPCILFLFYGW 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113 SGYLFLGYPADRFGRRGIVLLTLGLVGPCGVGGAAAGSSTGVMALRFLLGFLLAGVDLGV 172
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                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39 NFAAAIPGHRCWVHMLDNNTGSGNETGILSEDALLRISIPLDSNLRPEKCRRFVHPQWQL 98
                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               283 SST 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  225 TKT 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 ------DENHCLKDWDYNGLPVLTTNAIGQWDLVCDLGWQVILEQILFILGFA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99 LHLNGTIHSTSEADTEPCVDGWVYD-QSYFPSTIVTKWDLVCD--YQSLKSVVQFLL--- 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 HYGAFPPNASGW-EQPPNASGVSVASAALAASAASRVATSTDPS-----CSGFAPP---- 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 31/4 POI
CITY: Palo Alto
                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM CON OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/989,386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Corley, Neil C.
Shah, Purvi
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Guegler, Karl J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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650-845-4166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein
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US-09-031-392-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/09031392 Patent No. 5942398
                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
APPLICANT: Weng, Xun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/031,392
FILING DATE: 26-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Mciklejohn, Ph.D. Anita L.
REGISTRATION NUMBER: 35,283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
TEXTOR OF TAXABLE TO THE TAXABLE TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: NUCLEIC ACID MOLECULES
TITLE OF INVENTION: ENCODING GLUTEX AND USES THEREOF
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                   TELEFAX: UI.
                             LENGTH: 494 ...
Type: amino acid
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LENGTH: 581 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       131 ----GLIPPDATLYFDVVLLDVWNKADTVQS 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      195 ARTNGIKNAEETLNIEVVRSTMQEELDAAQT 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      137 LVCDYQSLKSVVQFL--LLTGMLVGGIIGGHVSDRWLVESARWLIITNKLDEGLKALRKV 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AMEDIA: GE...
LIBRARY: GE...
94162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89 -----AIVVGVGRLITGM-DRGLMGMCVNER-----RRLIVPPHLGYGSIGVA-- 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 -----PRACPREVQMGDFVRYHYNGTFE-----DGKKFDSSYDRSTLV---- 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78 PLDSNLRPEKCRREVH-PQWQLLHLNGTIHSTSEADTEPCVDGWVYDQSYFPSTIVTKWD 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19 LHLVFILPSLMLLIPHILLENFAAAIPGHRCWVHMLDNNTGSGNETGILSEDALL-RISI 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 6.2%; Score 87; DB 2; Length 581; Local Similarity 25.1%; Pred. No. 0.26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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                                                                                             494 amino acids
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; Sequence 5, Application US/09299549

; Patent No. 6136547
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FILING DATE: 26-FEB

ATTORNEY/AGENT INFORMATION:

NAME: Meiklejohn, Ph.D., Anita L.

REGISTRATION NUMBER: 35,283

REFERENCE/DOCKET NUMBER: 07334/0720

TELECOMMUNICATION INFORMATION:

"FT.EPHONE: 617/542-5070
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                                                                                                                                                                            Matches
                                                                                                                                                                          Best Local Similarity Matches 27; Conserv
                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                  TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 494 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: US/09/299,549
229 LWGTEDVAQDIQEMKDESMRMSQEKQV-----TVLELFRAPNYRQPIIISIMLQ 277
                                    194 VARTNGIKNAEETLNIEVVRSTMQEELDAAQTKTTVCDLFRNPSMRKRICILVFLR 249
                                                                             184 WPLLLGFTILPAIIQCAALP-------FCPESPRFLLINRKEEEKAKEILQR 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/031,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                    135 WDLVCDYQSLKSVVQFLLLTGMLVGGIIGGHVSDRWLVESARWLIITNKLDEGLK-ALRK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Tartaglia, Louis A.
APPLICANT: Weng, Xun
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING
TITLE OF INVENTION: GLUTEX AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 61//542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         194 VARTNGIKNAEETLNIEVVRSTMQEELDAAQTKTTVCDLFRNPSMRKRICILVFLR 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                184 WPLLLGFTILPAIIQCAALP-------FCPESPRFLLINRKEEEKAKEILQR 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      135 WDLVCDYQSLKSVVQFLLLTGMLVGGIIGGHVSDRWLVESARWLIITNKLDEGLK-ALRK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 26-APP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    229 LWGTEDVAQDIQEMKDESMRMSQEKQV-----TVLELFRAPNYRQPIIISIMLQ 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 02110-2804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 225 F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 5.9%; Score 83.5; DB 2; Length 494; l Similarity 23.3%; Pred. No. 0.52; 27; Conservative 26; Mismatches 40; Indels 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MΑ
                                                                                                                                                                                                                                                                                                                                                          494 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    225 Franklin Street
                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IBM Compatible
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GTR2_MOUSE
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GTR3_SHEEP
C11A_CAPHI
GTR1_CHICK
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C11A_HUMAN
MKK2_DROME
GTR1_MOUSE
GTR1_RABIT
GTR1_RAF
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GTR3_CHICK
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GTR1_HUMAN
GTR3_RABIT
YD56_YEAST
C11A_PIG
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C11A_HORSE
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YM31_MYCTU
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p28568 gallus gall
p77993 thermotoga
p58352 bos taurus
p47843 ovis aries
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p478153 capra hircu
p46896 gallus gall
Q92339 schizosacch
p11166 homo sapien
Q9xsc2 oryctolagus
Q04399 saccharomyc
p10612 sus scrofa
p53166 saccharomyc
p10612 sus scrofa
p53166 saccharomyc
Q50676 mycobacteri
p05108 homo sapien
p49071 drosophila
p17809 mus musculu
p13355 oryctolagus
p11167 rattus norv
Q9ept4 mesocricetu
Q09314 caenorhabdi
Q46515 equus cabal
p31431 homo sapien
Q10189 bos taurus
Q14651 homo sapien
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070594; 090WLO;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
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Organic cation/carnitine transporter 2 (Solute carrier family 22,
                 member 5) (High-affinity sodium-dependent carnitine
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TE; PS00216; SUGAR_TRANSPORT_1; 1.
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               cotransporter)
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                                                                                                                                                                                                                                                                                           modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-I- FUNCTION: SODIUM-ION DEPENDENT, HIGH AFFINITY CARNITINE
TRANSPORTER. ALSO TRANSPORTS ORGANIC CATIONS WITHOUT THE
INVOLVEMENT OF SODIUM. INVOLVED IN THE ACTIVE CELLULAR UPTAKE
                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDITINE-99384224; pubMed-10454528; Wu X., Huang W., Prasad P.D., Seth P., Rajan D.P., Leibach F.H., Chen J., Conway S.J., Ganapathy V., "Functional characteristics and tissue distribution pattern of organic cation transporter 2 (OCTN2), an organic cation/carnitine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochem. Biophys. Res. Commun. 251:586-591(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Molecular cloning and characterization of high-affinity carnitine transporter from rat intestine.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-SPRAGUE-DAWLEY; TISSUE-Intestine; MEDLINE-99011422; PubMed-9792817;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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SLC22A5 OR OCTN2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: EXPRESSED IN THE PROXIMAL AND DISTAL TUBULES
AND IN THE GLOMERULI IN THE KIDNEY, IN THE MYOCARDIUM, VALVES, ALARTERIOLES IN THE HEART, IN THE LABYRINTHINE LAYER OF THE
PLACENTA, AND IN THE CORTEX, HIPPOCAMPUS, AND CEREBELLUM IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY. ORGANIC
                                                                                                                                                                                                                                                                                                                                                                                                                        CATION SUBFAMILY.
                                                                                                                                                                                                     PS00216;
                                                                                                                                                                                                                            IPR003662; sub_transporter.
                                                                                                                                                                                  Transmembrane;
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   RESULT 3
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O76082;
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                                                                                                                                                                                              MEDITINE-98289574; PubMed-9618255; Wu X., Prasad P.D., Leibach F.H., Ganapathy V.; CDNA sequence, transport function, and genomic organization of human OCTN2, a new member of the organic cation transporter family."; Blochem. Biophys. Res. Commun. 246:589-595(1998).
                                                                                                                                                                                                                                                                                                                                                                     member 5) (High-affinity sodium-dependent carnitine cotransporter). SLC22A5 OR OCTN2.
                                                                                                                                                                                                                                                                                                                                                                                                  Organic cation/carnitine transporter 2 (Solute carrier family 22)
                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                        TISSUE=Kidney;
MEDLINE=98352077; PubMed=9685390;
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                          affinity human carnitine transporter OCTN2.", J. Biol. Chem. 273:20378-20382(1998).
                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                MEDLINE=99113835; PubMed=9916797;
                                SEQUENCE FROM N.A.
                                                                                            Molecular and functional identification of sodium ion-dependent, high
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NNTGSGNETGILSEDALLRISIPL---DSNLRPEKCRRF---VHPQWQLLHLN-GTIHST 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SQGRVKEAEVIIRKAAKFNGI------VAPSTIFDPSELQDLNSKKPQSHHIYDLV 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RFGRKNVLELTMGMQTGFSFLQLFSVNFEMFTVLFVLVGMGQISNYVAAFVLGTEILSKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ITNKLDEGLKALRKVARTNGIKNAEETLNIEVVRSTM--QEELDAAQTKTT----VCDLF 233
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J., Tamai I.,
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91
275
557
                                                                                                                       Ohashi R., Nezu J.-I., Yabuuchi H., Oku A., Shimane
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                                                                                                                                                                                                                                                                                                                                                           (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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22.7%;
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    Ohashi R.,
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N-LINKED (GLCNAC. . .) (POTENTIAL).
W -> G (IN REF. 2).
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Pred. No. 8.6e-10;
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      Yabuuchi H.,
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        Hashimoto N.,
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Yashino M., Kato H., Ohura T., Tsujimoto G., Hayakawa J., Shimane M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        deficiency: a novel Arg169Gln mutation and a recurrent Arg282ter mutation associated with an unconventional splicing abnormality.
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Gerbitz K.-D., Kilimann M.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen J., Conway S.J., Ganapathy V., "Functional characteristics and tissue distribution pattern of organic cation transporter 2 (OCTN2), an organic cation/carnitine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wu X., Huang W., Prasad P.D., Seth P., Rajan D.P., Leibach F.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Primary systemic carnitine deficiency is caused by mutations in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tang N.L., Ganapathy V., Wu X., Hui J., Seth P., Yuen P.M., Wanders R.J., Fok T.F., Hjelm N.M.;
"Mutations of OCTN2, an organic cation/carnitine transporter, lead to deficient cellular carnitine uptake in primary carnitine deficiency.";
Hum. Mol. Genet. 8:655-660(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Identification of two novel mutations in OCTN2 of three patients with systemic carnitine deficiency.";
Hum. Genet. 105:157-161(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99384224;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transporter."
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Rodrigues Pereira R., Schweitzer S., de Klerk J.B.C., W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochem. Biophys. Res. Commun. 261:484-487(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organic cation transport function and the carnitine transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Mutations in novel organic cation transporter (OCTN2), an org
cation/carnitine transporter, with differential effects on the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHARACTERIZATION OF VARIANT CDSP LEU-478, AND MUTAGENESIS. MEDLINE=20026865; PubMed=10559218;
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MEDLINE-99172075; PubMed-10072434;
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                                                                                                                                                                                                                                                                            "Two novel missense mutations of the OCTN2 gene (W283R and V446F) in patient with primary systemic carnitine deficiency."; Hum. Mutat. 15:118-118(2000).
                                                                                                                                                                                                                                                                                                                                                   Mayatepek E., Nezu J., Tamai I., Oku A., Katsura M., Shimane M.,
                                                                                                                                                  carnitine transport activity."; Hum. Mutat. 15:238-245(2000).
                                                                                                                                                                                 Wang Y., Kelly M.A., Cowan T.M., Longo N.; "A missense mutation in the OCTN2 gene associated with residual
                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20081068; PubMed=10612840;
                                                                                                                                                                                                                                                                                                                                                                                             VARIANTS CDSP ARG-283 AND PHE-446
                                                                                                                                                                                                                           VARIANT CDSP LYS-452.
MEDLINE=20145665; PubMed=10679939;
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                                                                                                              FUNCTION: SODIUM-ION DEPENDENT, HIGH AFFINITY CARNITINE TRANSPORTER. ALSO TRANSPORTS ORGANIC CATIONS WITHOUT THE
DISEASE: DEFECTS IN SLC22A5 ARE THE CAUSE OF SYSTEMIC PRIMARY
                                     TISSUE SPECIFICITY: STRONGLY EXPRESSED IN KIDNEY,
                 HEART AND PLACENTA.
                                                         SUBCELLULAR LOCATION: Integral membrane protein
                                                                               CARNITINE
                                                                                          INVOLVEMENT OF SODIUM. INVOLVED IN THE ACTIVE CELLULAR UPTAKE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wu X., Huang W., Leibach F.H., Ganapathy V.
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                                               SKELETAL MUSCLE
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                        61
                                                                               59
                                                                                                                                                                Local Similarity
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                                                                                                                      3 FEELLSQVGGLGRFQMLHLVFILPSLMLLIPH---ILLENFAAAIPGHRCWVHMLDN-NT 58
                       DTEPCVDGWVYDQSYFPSTIVTKWDLVCDYQSLKSVVQFLLLTGMLVGGIIGGHVSDR-- 169
                                               AWRNHT------VPLRLRDGREVPHSCRRYRLATIANFSALGLEPGRDVDLGQL
                                                                      GSGNETGILSEDALLRISIPL---DSNLRPEKCRRF---VHPQWQLLHLN-GTIHSTSEA 111
                                                                                                YDEVTAFLGEWGPFQ--RLIFFLLSAS-IIPNGFTGLSSVFLIATPEHRCRVPDAANLSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARNITINE DEFICIENCY (CDSP). CDSP IS AN AUTOSOMAL RECESSIVE DISORDER OF FATTY ACID OXIDATION CAUSED BY DEFECTIVE CARNITINE TRANSPORT. PRESENT EARLY IN LIFE WITH HYPOKETOTIC HYPOGLYCEMIA ACUTE METABOLIC DECOMPENSATION, OR LATER IN LIFE WITH SKELETAL MYOPATHY OR CARDIOMYOPATHY.
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                                                                                                                                                                                                               557 AA;
                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transmembrane; Glycoprotein; Disease mutation.
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                                                                                                                                                          13.8%; Score 193.5; DB 1
22.0%; Pred. No. 1.3e-09;
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                                                                                                                                                                                                                     M->R: LOSS OF BOTH CARNITINE AND ORGANIC CATION TRANSPORT FUNCTIONALITIES.
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POTENTIAL.
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Multigene family; Polymorphism

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  InterPro; IPR003663; Sugar_transporter.
InterPro; IPR003662; sub_transporter.
Pfam; PP00083; sugar_tr; 1.
PRINTS; PR00171; SUGATRINSPORT.
PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.
PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
Transmembrane; Sugar_transport; Transport; Glycoprotein;
                                                                                                                                                                                                              MIM; 138160;
                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-s
                                                                                                                                                                                                                                                            EMBL; J03810; AAA59514.1; -.
                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
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01-JUL-1989 (Rel. 11, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Solute carrier family 2, facilitated glucose transporter, member 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Liver, and Kidney;
MEDLINE=88289735; PubMed=3399500;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTESTINE, AND KIDNEY. SIMILARITY: BELONGS TO
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p14246; Q9DBA7;
01-JAN-1990 (Rel. 13, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Solute carrier family 2, facilitated glucose transporter,
                                                                                                                                                                                                                                                                                                                                                                                                                           MOUSE
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                                                                                                                                                                                                                                                                          (Glucose transporter type 2, liver). SLC2A2 OR GLUT2 OR GLUT-2.
                                                                                                                          SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-Liver;
MEDLINE-90098776; PubMed-2602116;
                                                                                                                                                                                                                                                        Mus musculus (Mouse).
                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                            Suzue K.,
                                                                                                                                                                                                  NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                149 QFLLLTGMLVGGIIG-----GHVSDRWLV------ESARWLIITNK 183
                                                                         Nucleic Acids
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MEDLINE=89366666; PubMed=2771649;
                                  SEQUENCE FROM N.A.
                                                                                         Sequence
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35; Conserv
                                                                       Lodish H.F., Thorens B.;
of the mouse liver glucose transporter.";
cids Res. 17:10099-10099(1989).
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                   TISSUE-Liver;
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1 (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
7 (POTENTIAL).
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4 (POTENTIAL).
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3 (POTENTIAL
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2 (POTENTIAL).
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12 (POTENTIAL).
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DA600577207EC083 CRC64;
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EMBL; X16986; CAA34855.1; -.
EMBL; X15684; CAA33719.1; -.
EMBL; S77926; AAB20847.1; -.
EMBL; AK005068; BAB23792.1; -.

MGI:1095438; Slc2a2. \$06920; \$06920 \$05319; \$05319

IPR003663; Sugar\_transporter

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RA AIZAWA K., IZAWA M., NISHI K., KIYOSAWA H., KONDO S., Yamanaka I., Ra Aizawa K., IZAWA M., NISHI K., KIYOSAWA H., KONDO S., Yamanaka I., Ra Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Ra Fleischmann W., Gaasterland T., Gissi C., King H., Kochiwa H., RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., RA Sakai K., Okido T., Frunon M., Aono H., Baldarelli R., Barsh G., Sakai K., Okido T., Frunon M., Aono H., Baldarelli R., Barsh G., RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H., RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., RA Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Asano T., Shibasaki Y., Lin J.L., Akanuma Y., Takaku F., Oka Y. The nucleotide sequence of cDNA for a mouse liver-type glucose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 384-496 FROM N.A.

MEDLINE-92111400; PubMed-1765007;
Hogan A., Heyner S., Charron M.J., Copeland N.G., Gilbert D.J.
Jenkins N.A., Thorens B., Schultz G.A.;
"Glucose transporter gene expression in early mouse embryos.";
Development 113:363-372(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Differential screening of a PCR-generated mouse embryo cDNA library: glucose transporters are differentially expressed in early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Smith D.E., Gridley T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-93170163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Development 116:555-561(199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      postimplantation mouse embryos.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: FRACILITATIVE GLUCOSE TRANSPORTER. THIS ISOFORM LIKELY MEDIATES THE BIDIRECTIONAL TRANSFER OF GLUCOSE ACROSS THE PLASMA MEDBARAE OF HEBATOCYTES AND IS RESPONSIBLE FOR UPTAKE OF GLUCOSE BY THE BETA CELLS; MAY COMPRISE PART OF THE GLUCOSE-SENSING MECHANISM OF THE BETA CELL. MAY ALSO PARTICIPATE WITH THE MECHANISM OF THE BETA CELL. MAY ALSO PARTICIPATE WITH THE NA(+)/GLUCOSE COTRANSPORTER IN THE TRANSCELLULAR TRANSPORT OF GLUCOSE IN THE SMALL INTESTINE AND KIDNEY.
SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: IN EMBRYO, EXPRESSED IN ENDODERM LAYER OF YOLK SAC AND LIVER PRIMORDIUM.
SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY GINCOSE SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY GINCOSE
                                                                                                                                                                                                                                                                                                                                                                                            TRANSPORTER SUBFAMILY.
                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on it by non-profit institutions as long as its content is in no was by non-profit institutions as long as its content.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yoshino M., Itoh M., Ishii Y.,
Konno H., Adachi J., Fukuda S.,
Sawa H., Kondo S., Yamanaka I.,
Bono H., Kasukawa T., Saito R.,
                                                                                                                                                                                                                                                                                                                                       a collaboration
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RESULT 6
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Matches
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                                                                                                16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
CYtochrome P450 11A1, mitochondrial precursor (EC 1.14.15.6) (CYPXIA1)
(P450(scc)) (Cholesterol side-chain cleavage enzyme) (Cholesterol
                                     CYP11A OR CYP11A1.
Mus musculus (Mouse).
Eukaryota; Metazoa; C
       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                Q9QZ82;
                                                                                                                                                                                                                                                                 C11A_MOUSE
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PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
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PRINTS; PR00171; SUGRTRNSPORT.
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Pfam; PF00083; sugar_tr; 1.
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32
98
119
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25.6%;
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CYTOPLASMIC (POTENTIAL).

N-LINKED (GLUAC. . .) (PC
G -> D (IN REF. 2).
T -> N (IN REF. 1).
S -> T (IN REF. 2).
F -> L (IN REF. 1).
P -> S (IN REF. 1).
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Pred. No. 0.65;
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                                                                                                                                                                                                                                                              PRT;
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9 (POTENTIA
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CYTOPLASMIC (
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                                                                                             GTR2_RAT
P12336;
01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Solute carrier family 2, facilitated glucose
(Glucose transporter type 2, liver).
SLC2A2 OR GLUT2 OR GLUT-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BINDING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tanaka M., Hennebold J.H., Adashi E.Y.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
-i-FUNCTION: CATALYZES THE SIDE-CHAIN CLEAVAGE REACTION OF
CHOLESTEROL TO PREGNENOLONE (BY SIMILARITY).
-i-CATALYTIC ACTIVITY: Cholesterol + reduced adrenal ferredoxin +
                                                                                                                                                                                                                      228 TVCDL-FRN 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Steroidogenesis; Transit peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oxidoreductase; Monooxygenase; Membrane; Heme; Mitochondrion;
                                                                                                                                                                                        394 TVNDLVLRN 402
                                                                                                                                                                                                                                                                                                           283 -WDLRQKRDFSQYPGVLYSLLGGNKLPFKNIQANITEMLAGGVDTTSMTLQWNLYEMAHN 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00086;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF195119; AAF03897.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 O(2) = pregnenolone + 4-methylpentanal + oxidized adrenal ferredoxin + H(2)O.
-i- PATHWAY: INITIAL RATE-LIMITING REACTION IN THE SYNTHESIS VARIOUS STEROID HORMONES.
                                                                                                                                                                                                                                                                                                                                                                        237 MFHTSVPMLNLPPDFFRLLRTKTWKDHAAAWDVIFNKADE-----YTQNFY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                  179
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                  98 LLHLNGTI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 VHMLDNNTGSGNETGILSEDALLRISIP------LDSNLRPEKCRRFVHPQWQ 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                           7
                                                                                                                                                                                                                                                                                                                                         KWDL---VCDYQSLKSVVQFLL-------LTGMLVGGIIGGHVSDRW-LVESARW
                                                                                                                                                                                                                                             LKVQEMLRAEVLAARRQAQGDMAKMVQLVPLLKASIKETLRLHPISVTLQ-----RY 393
                                                                                                                                                                                                                                                                           LIITNKLDEGLKALRKVARTNGIK------NAEETLNIEVVRSTMQEELDAAQTKT 227
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rPro; IPR001128; Cy
FF00067; p450; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                            STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOCHROME_P450; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.7%;
22.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60314 MW; E5029738EE4ECB71 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 93.5; DB pred. No. 0.88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                        522 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                          transporter, member 2
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MEDILINE-89003066; PubMed-3048704;
Thorens B., Sarkar H.K., Kaback H.R., Lodish H.F.;
"Cloning and functional expression in bacteria of a novel glucose
transporter present in liver, intestine, kidney, and beta-pancreatic
islet cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell 55:281-290(1988)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A31556; A31556.
InterPro; IPR003663;
InterPro; IPR003662;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00083;
                                                                                                                                                                                                                                                                                                                                                                                                 prosite; ps00216; sugar_transport_1; 1.
prosite; ps00217; sugar_transport_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                    Transmembrane; Sugar transport; Transport; Glycoprotein;
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SEQUENCE
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                                                                   TRANSMEM
                                                                                 DOMAIN
                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: FACILITATIVE GLUCOSE TRANSPORTER. THIS ISOFORM LIKELY MEDIATES THE BIDIRECTIONAL TRANSFER OF GLUCOSE ACROSS THE PLASMA MEMBRANE OF HEPATOCYTES AND IS RESPONSIBLE FOR UPTAKE OF GLUCOSE BY THE BETA CELLS; MAY COMPRISE PART OF THE GLUCOSE-SENSING MECHANISM OF THE BETA CELL. MAY ALSO PARTICIPATE WITH THE NA(+)/GLUCOSE COTRANSPORTER IN THE TRANSCELLULAR TRANSPORT OF GLUCOSE IN THE SMALL INTESTINE AND KIDNEY.

GLUCOSE IN THE SMALL INTESTINE AND KIDNEY.

SUBCELLULAR LOCATION: INCEGING INCEDENCY AND BETA-PANCREATIC ISLET CELLS.

SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY. GLUCOSE SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSPORTER SUBFAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                            PR00171
                                                                                                         237
302
323
338
359
366
387
                                                                                                                                                                                                                                                                                                                                                                                                                            sugar_tr; 1.
1; SUGRTRNSPORT
                                                                                 sub_transporter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sugar_transporter.
    57085 MW;
  N-LINKED (GLCNAC. . .) (P
075AB81E56CF33F7 CRC64;
                                                                                                                                                                                            CYTOPLASMIC
                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                   CYTOPLASMIC
5 (POTENTIA)
                                                                                                                                                                                                                                                              EXTRACELLULAR (POTENTIAL).
4 (POTENTIAL).
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3 (POTENTIAL
                                                                                                                                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL)
2 (POTENTIAL).
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                                         EXTRACELLULAR (POTENTIAL)
12 (POTENTIAL)
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CYTOPLASMIC (P
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                               CYTOPLASMIC (POTENTIAL)
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                    (POTENTIAL).
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Query Match

6.6%;

Score

DΒ

Length 522;

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IN FKBX_MOUSE
IN FKBX_MOUSE
IN FKBX_MOUSE
DT 30-MAY
DT 30-MAY
DT 16-CCT
RR SIMEK
RR SIMEK
RR SIMEK
RR SIRALIN
RR SEQUEN
RC STRALIN
RA SIMEK
RT Chrome
RT Chrome
RT Genomi
RN [2]
RN [2]
RN [2]
RN [2]
RN [2]
RN FITTON
RA SIMEK
RT STRALIN
RA SIMEK
RT Chrome
RT Chrome
RT Genomi
RN [2]
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30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
65 kDa FK506-binding protein precursor (EC 5.2.1.8) (FKBP65) (FKBPRP)
(Peptidy)-proly1 cis-trans isomerase) (PPiase) (Rotamase)
(Immunophilin FKBP65).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FKBX_MOUSE
Q61576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Coss M.C., Winterstein D., Sowder R.C. II, Simek S.L.;
"Molecular cloning, DNA sequence analysis, and biochemical
characterization of a novel 65-kba FK506-binding protein (FKBP65).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-JB6; TISSUE-Epidermis;
MEDLINE-94117013; PubMed-7507077;
Simek S.L., Kozak C.A., Winterstein D., Hegamyer G.,
"Sequence and localization of a novel FK506-binding p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FKBP6 OR FKBP1-RS OR FKBP-RS OR FKBPRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chromosome 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genomics 18:407-409(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     296
                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=96094328; PubMed=7493967;
MGD; MGI:104769; Fkbp6.
InterPro; IPR002048; EF-hand.
InterPro; IPR000886; ER_target
                                                                                  HSSP;
                                                                                     EMBL; L07063; AAC37678.1; -. HSSP; P20081; 1YAT.
                                                                                                                                                                                                                                                                                                                         between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN SYNTHESIS.

CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PSMRKRICILVFL 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIITNKLDEGLKALRKVARTNGIKNAEETLNIEVVRSTMQEELDAAQT--KTTVCDLFRN 235
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                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                       PTM: GLYCOSYLATED AND PHOSPHORYLATED. SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY. CONTAINS 4 FKBP-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS DURING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PNYROPIVVALML 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE SPECIFICITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENZYME REGULATION: INHIBITED BY BOTH FK506 AND RAPAMYCIN, BUT NOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AND TESTIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY CYCLOSPORINE A.
                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                            the Swiss Institute of Bioinformatics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  270:29336-29341(1995)
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                                                                                                                                                                                                                                                                                                                                  and the EMBL outstation
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Best Local
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                                                                                                                                          GTR3_CHICK STANDAKU;

GTR3_CHICK STANDAKU;

P28568;

01-DEC-1992 (Rel. 24, Created)

01-DEC-1992 (Rel. 24, Last sequence update)

01-MAR-2002 (Rel. 41, Last annotation update)

Solute carrier family 2, facilitated glucose transporter, member
"Differential regulation of glucose transporter isoforms oncogene in chicken embryo fibroblasts."; Mol. Cell. Biol. 11:4448-4454(1991).
                                       SEQUENCE FROM N.A. MEDLINE=91342646; PubMed=1875932; White M.K., Rall T.B., Weber M.J.;
                                                                                                                    Archosauria; Aves; Neognathae;
                                                                                                                               Eukaryota; Metazoa;
                                                                                                                                                                                                                                                           CHICK
                                                                                             NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                    131 ----GLIPPDATLYFDVVLLDVWNKADTVQS 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                           195 ARTNGIKNAEETLNIEVVRSTMQEELDAAQT 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00018; EF_HAND; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00453; FKBP_PPIASE_1; FALSE_NEG.
PROSITE; PS00454; FKBP_PPIASE_2; 1.
PROSITE; PS50059; FKBP_PPIASE_3; 4.
PROSITE; PS00014; ER_TARGET; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Endoplasmic
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Pfam; PF00254; FKBP; 4.
SMART; SM00054; EFh; 2.
                                                                                                                                                                                                                                                                                                                                                                                 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                78
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                                                                                                                                                                                                                                                                                                                                                -----AIVVGVGRLITGM-DRGLMGMCVNER-----RRLIVPPHLGYGSIGVA--
                                                                                                                                                                                                                                                                                                                                                                        LVCDYQSLKSVVQFL--LLTGMLVGGIIGGHVSDRWLVESARWLIITNKLDEGLKALRKV 194
                                                                                                                                                                                                                                                                                                                                                                                                 -----PRACPREVQMGDFVRYHYNGTFE------DGKKFDSSYDRSTLV----
                                                                                                                                                                                                                                                                                                                                                                                                                       PLDSNLRPEKCRRFVH-PQWQLLHLNGTIHSTSEADTEPCVDGWVYDQSYFPSTIVTKWD 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                    LHRVRILPLLLLL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rotamase; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         reticulum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ÃΑ;
                                                                                                             Chordata; Craniata; Vertebrata; Euteleostomi;
Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64669 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.2%; Score 87; DB 1; Length 581; 25.1%; Pred. No. 3.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    speat; Glycoprotein; Signal; Phosphorylation;
Calcium-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                -----QTLERGLGRASPAGAPLEDVVIERYHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PREVENT SECRETION FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPIASE, FKBP-TYPE 4.
EF-HAND 1 (POTENTIAL).
EF-HAND 2 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPIASE, FKBP-TYPE
PPIASE, FKBP-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
65 KDA FK506-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1B51B3032089F555 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FKBP-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GLCNAC. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL). (POTENTIAL). (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ER (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
                           by
                                                                                                             Phasianinae;
                           the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68;
                           src
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10;
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RESULT 10
GYRB_THEMA
                                                                                                                                                                                                       Qy
                                                                                                                                                                                                                                                     Вb
                                                                                                                                                                  Вb
                                                                                                                                                                                                                                                                                            γ
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SON THE PROPERTY OF THE PROPER
                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                             Matches
                           GYRB_THEMA P77993;
30-MAY-2000 (Rel. 39, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
SEQUENCE
                                                                                                                                                                                           195 ARTNGIKNAEETLNIEVVRSTMQEELD--AAQTKTTVCDLFRNPSMRKRICILVFLR 249
                                                                                                                                                 228 QKLRGTQDVSQDI-----SEMKEESAKMSQEKKATVLELFRSPNYRQPIIISITLQ
                                                                                                                                                                                                                                              185 WPLLLGFTIVPAVLQCVALL---
                                                                                                                                                                                                                                                                                 135 WDLVCDYQSLKSVVQFLLLTGMLVGGIIGGHVSDRWLVESARWLIITNKLDEGLKALRKV 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A41264; A41264.
InterPro; IPR003563; Sugar_transporter.
InterPro; IPR003662; sub_transporter.
Pfam; PF00083; Sugar_tr; 1.
PRINTS; PR00171; SUGETRNSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Multigene
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.
PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transmembrane; Sugar transport; Transport; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- FUNCTION: FACILITATIVE GLUCOSE TRANSPORTER. PROBABLY A NEURONAL GLUCOSE TRANSPORTER.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY. GLUCOSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M37785; AAA48662.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSPORTER SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 496
                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28
66
87
95
116
126
147
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA;
                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54174 MW;
                                                                                                                                                                                                                                                                                                                               6.2%; Score 86.5; D) 26.5%; Pred. No. 3.4; tive 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 (POTENTIAL)
CYTOPLASMIC (1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (
                                                                                                                                                                                                                                       N-LINKED (GLCNAC. . .) (P 75B3C0F61A7A92A5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
12 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEFINES SUBSTRATE SPECIFICITY (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OYTOPLASMIC

9 (POTENTIA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL)
8 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (
5 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL).
2 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
                                              636
                                            A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          There are no restrictions on ong as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
                                                                                                                                                                                                                                                                                                                               25;
                                                                                                                                                      278
                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                             5
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Best Local Similarity
                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genome sequence of Thermotoga maritima.";

Nature 399:323-329(1999).

NATURE THANDED DIA IN AN ATP-DEPENDENT MANNER AND ALSO CATALYZES THE STRANDED DIA IN AN ATP-DEPENDENT MANNER AND ALSO CATALYZES THE INTERCONVERSION OF OTHER TOPOLOGICAL ISOMERS OF DOUBLE-STRANDED DIA RINGS, INCLUDING CATEANAMES AND KNOTTED RINGS.

-!- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining of double-stranded DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAY-2000 (Rel. 39, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation updat DNA gyrase subunit B (EC 5.99.1.3) (Topoiso GYRB OR TOP2B OR TM0833.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A., McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M., Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D., Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O., Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M., Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M., William C., Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M., White O., Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M., White O., Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M., White O., Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M., White O., Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M., White O., Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M., White O., Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M., White O., Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M., White O., Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M., White O., Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M., White O., Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M., White O., Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M., White O., Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M., White O., Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M., White O., White
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=MSB8 / DSM 3109;
MEDLINE=97017137; PubMed=8863738;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thermotoga maritima.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Guipaud O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-99287316; PubMed-10360571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-MSB8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene 174:121-128(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               maritima."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=2336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                         Pfam; PF00986; DNA_gyraseB_C; 1.
Pfam; PF00204; DNA_topoisoII; 1.
Pfam; PF02518; HATPase_C; 1.
Pfam; PF01751; Toprim; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U49692; AAC44498.1; -. EMBL; AE001750; AAD35915.1;
                                                                                                                                                                                     SMART; SM00387; HATPASe_C; 1.
SMART; SM00433; TOP2C; 1.
pROSITE; PS00177; TOPOISOMERASE_II; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP;
                                                                                                                                                                                                                                                        Prodom; PD149633; DNA_gyraseB_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                             PRINTS; PRO0418; TPI2FAMILY.
                                                                                                                                                              Isomerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ipaud O., Labedan B., Forterre P.;
gyrB-like gene from the hyperthermophilic bacterion Thermotoga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: MADE UP OF TWO CHAINS. THE A CHAIN IS RESPONSIBLE FOR DNA BREAKAGE AND REJOINING; THE B CHAIN CATALYZES ATP HYDROLYSIS. THE ENZYME FORMS AN A2B2 TETRAMER.
SIMILARITY: BELONGS TO THE TYPE II TOPOISOMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P06982; 1AJ6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TM0833;
                                                                                                                                                                                                                                                                                             PD000616; DNA_topoisoII;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thermotogales; Thermotoga.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR001241; DNA_topoisoII.
IPR003594; HATPase_c.
IPR004359; HIS_KIN_sig.
IPR002936; Toprim.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR002288; DNA_gyraseB_C.
                                                                                                                                    Topoisomerase; ATP-binding; Complete proteome 152 152 V -> M (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / DSM 3109;
                                                                                                             636 AA;
                                                                                                             72427 MW;
6.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  st annotation update)
5.99.1.3) (Topoisomerase II subunit B).
                            Score
     Pred.
                                                                                                             B21E0E0CBEC6F89E CRC64;
  No.
     84.5;
No. 7;
                               DB 1;
                            Length 636;
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTR3_BOVIN STANDARD; PRT; 494 AA.
P58352;
01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Solute carrier family 2, facilitated glucose transporter, member 3
(Glucose transporter type 3, brain).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLC2A3 OR GLUT3
                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                Augustin R., Navarrete-Santos A., Fischer B.;
"Expression of glucose transporters amongst ruminants.";
submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9913;
                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                             -!- FUNCTION: FACILITATIVE GLUCOSE TRANSPORTER. PROBABLY A NEURONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rissuE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Augustin R., Fischer B.; "Glucose transporter expression during bovine preimplantation embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               236 VIHIKRTEKVKTKNGEDEVIVEIAFQYTDSYSEDIVSFANTIKTV 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  194 V---ARTNGI--KNAEETLNIEV----VRSTMQEELDAAQTKTTV 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106 HSTSE-ADTEPCVDGWVYDQSYFPSTIVTKWDLVCDYQSLKSVVQF------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 385-494 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 VGGLGRFQMLHLVFILPSLMLLIPHILLENFAAAIPGHRCWVHMLDNNTGSGNETGILSE
                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY. GLUCOSE
                                                                                                                                                                                                                                                                                                                          TRANSPORTER SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                              GLUCOSE TRANSPORTER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IGSTGKRGLHHLVY------EVVDNSVDEALAGYCDWIRV-----TLHE
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                                                                                                                                             AY033938; AAK70222.1; -.
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prosite; ps00216; sugar\_transport\_1; 1.
prosite; ps00217; sugar\_transport\_2; 1.

AF308829;

AAK63202.1; -

Transmembrane; Sugar transport; Transport; Glycoprotein;

DOMAIN

Multigene family.

DOMAIN

TRANSMEM

26 64

I (POTENTIAL).
EXTRACELLULAR (POTENTIAL) CYTOPLASMIC (POTENTIAL).

(POTENTIAL)

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RESULT
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Best Local
MEDIINE-97392487; PubMed-9250701;
Currie M.J., Bassett N.S., Gluckman P.D.;
"Ovine glucose transporter-1 and -3: cDNA partial sequences and
developmental gene expression in the placenta.";
                                                                                                       Bennett B.L., Prosser C.G., Grigor M.R., "Isolation of cDNAs and tissue specific expression of ovine glucose transporters.";
                                                                                                                                                                                           Ovis aries (Sheep).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Caprinae; Ovis.

NCBI_TaxID=9940;
                                                                                                                                                                                                                                              01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Solute carrier family 2, facilitated glucose transporter, member 3
Glucose transporter type 3, brain).
SLC2A3 OR GLUT3 OR GLUT-3.
                                                       TISSUE=Placenta;
                                                                 SEQUENCE OF 88-248 FROM N.A.
                                                                                                                                       STRAIN-COOPWORTH;
MEDLINE-96109471; PubMed-8653093;
                                                                                          Biochem. Mol. Biol. Int. 37:9-16(1995)
                                                                                                                                                                                                                                                                                                                                                         SHEEP
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CARBOHYD
                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                184 WPLLLGFTILPAIIQCAALP------FCPESPRFLLINRKEEEKAKEILQR 228
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Pred. No. 6.3;
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9 (POTENTIAL
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N-LINKED (GLCNAC. . .) (POTENTIAL).
PWFIV -> SLYYC (IN REF. 2).
EC42A3C648CAD23C CRC64;
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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SEQUENCE
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EMBL: U89030; AAB49313.1; ...
InterPro; IPR003663; Sugar_transporter.
InterPro; IPR003662; sub_transporter.
Pfam; PF00083; sugar_tr; 1.
PRINTS; PR00171; SUGERTRNSPORT.
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                                                                                                                 229 LWGTEDVAQDIQEMKDESMRMSQEKQV-----TVLELFRAPNYRQPIIISIMLQ
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PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
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-!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN.
-!- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY. GLUCOSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Placenta 18:393-401(1997).
-!-- FUNCTION: FACILITATIVE GLUCOSE TRANSPORTER. PROBABLY A NEURONAL
                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSPORTER SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLUCOSE TRANSPORTER.
                                                                                                                                                                                                                                                                                                                            27;
                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       494
                                                                                                                                                                                                                                                                                                                            Conservative
     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sugar transport; Transport; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                5.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  43
54194
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MW;
                                                                                                                                                                                                                                                                                                                      ; Score 83.5; D;; Pred. No. 6.3; 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 (POTENTIAL).
CYTOPLASMIC (P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL).
DEFINES SUBSTRATE SPECIFICITY (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL)
8 (POTENTIAL)
  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 (POTENTIAL)
CYTOPLASMIC (
9 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL) 6 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL)
2 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           L2 (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                     A89204D3EA74BFBA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
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                                                                                                                                                                                                                     -----FCPESPRFLLINRKEEEKAKEILQR 228
520 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                      40;
                                                                                                                                                                                                                                                                                                                                                                     Length 494;
                                                                                                                                                                                                                                                                                                                      Indels
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Best Local
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
Cytochrome P450 11A1, mitochondrial precursor (EC 1.14.15.6) (CYPXIA1)
(P450(sec)) (Cholesterol side-chain cleavage enzyme) (Cholesterol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDITINE-96244421; Pubmed-8645627;
MEDITINE-96244421; Pubmed-8645627;
Okuyama E., Okazaki T., Furukawa A., Wu R.-F., Ichikawa Y.;
Okuyama E., Okazaki T., Furukawa A., Wu R.-F., Ichikawa Y.;
Okuyama E., Okazaki T., Furukawa A., Wu R.-F., Ichikawa Y.;
Okuyama E., Okazaki T., Furukawa A., Wu R.-F., Ichikawa Y.;
Okuyama E., Okazaki T., Furukawa A., Wu R.-F., Ichikawa Y.;
Okuyama E., Okazaki T., Furukawa A., Wu R.-F., Ichikawa Y.;
Okuyama E., Okazaki T., Furukawa A., Wu R.-F., Ichikawa Y.;
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Okuyama E., Okazaki T., Furukawa A., Wu R.-F., Ichikawa Y.;
Okuyama E., Okazaki T., Furukawa A., Wu R.-F., Ichikawa Y.;
Okuyama E., Okazaki T., Furukawa A., Wu R.-F., Ichikawa Y.;
Okuyama E., Okazaki T., Furukawa A., Wu R.-F., Ichikawa Y.;
Okuyama E., Okazaki T., Furukawa A., Wu R.-F., Ichikawa Y.;
Okuyama E., Okazaki T., Furukawa A., Wu R.-F., Ichikawa Y.;
Okuyama E., Okazaki T., Ichikawa Y.;

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Mammalia; Eutheria; Cetar
Bovidae; Caprinae; Capra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; D50058; BAA08776.1; -. HSSP; P00189; 1SCC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way use by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Capra hircus (Goat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            desmolase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Adrenal cortex;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oxidoreductase; Monooxygenase; Membrane; Heme; Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00067; p450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Steroidogenesis; Transit peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
373 VPLLKASIKETLRLHPISVTLQ 394
                                                                                                                                                                                                                              261
                                                                                                                                                                                                                                                                                                                                             204
                                                                                                                                                                                                                                                                                    94
                                                                                                                                                                                                                                                                                                                                                                                                34 HILLENFAAAIPGHRCWVHMLDNNTGSGNETGILSEDALLRISIPLDSNLRPEKCRRFVH 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHOLESTEROL TO PREGNENOLONE.

CATALYTIC ACTIVITY: Cholesterol + reduced adrenal ferredo:

O(2) = pregnenolone + 4-methylpentanal + oxidized adrenal

ferredoxin + H(2)O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Mitochondrial. SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PATHWAY: INITIAL RATE-LIMITING REACTION IN THE SYNTHESIS VARIOUS STEROID HORMONES.
                                                                                                                                                                                                                              KTWR-DHVAAWDTIFNKAEKYTE-----IFYQDLRQKTEFRNYPGIL-YHLLKSEKMLL
                                                                                                                                                                                                                                                                              POWOLLHING--TIHSTSEADTEPCVDGWVYDQSYFPSTIVTKWDLVCDYQSLKSVVQFL 151
                                                                                                               EDVKANITEMLAGGVDTTSMTLQWHLYEMARSLNVQEMLREEVLNARRQAEGDISKMLQM
                                                                                                                                                                                                                                                                                                                                          HFAFESITNVMFGER--LGMLEDTVNTEAQKFIDAVYKMFHTSVPL-LNLPPELYRLFRT 260
                                                                                                                                                                  ----LLTGMLVGGIIGGHVSDRW-LVESARWLIITNKLDEGLKALRKVARTNGIK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PR00385; P450.
; PS00086; CYTOCHROME_P450; 1.
                                                      ---NAEETLNIEVVRSTMQ 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR001128; Cyt_P450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 461
520 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     461 HI
60418 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.9%;
25.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOCHROME P450 11A1.
HEME (BY SIMILARITY).
; 4FB09A3C89310317 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 83.5; DB 1; Length 520; Pred. No. 6.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MITOCHONDRION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ferredoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wagstaff P., Kang H.Y., Mylott D., Robbins P.J., White M.K.; "Characterization of the avian GLUT1 glucose transporter: differential regulation of GLUT1 and GLUT3 in chicken embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=96157892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Glucose transporter type 1) (GT1). SLC2A1 OR GLUT1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00083; sugar_tr; 1.
PRINTS; PR00171; SUGRTRNSPORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; L07300; AAB02037.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fibroblasts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
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     DOMAIN
                                                                                                                       TRANSMEM
                                                                                                                                                                                               DOMAIN
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                                                                                                                                                                                                                                             DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003663; Sugar_transporter.
InterPro; IPR003662; sub_transporter.
                                                   DOMAIN
                                                                       TRANSMEM
                                                                                                   DOMAIN
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                                                                                                                                                                        TRANSMEM
                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Integral membrane protein. Localizes primarily at the cell surface (By similarity). SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY. GLUCOSE TRANSPORTER SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . Biol. Cell 6:1575-1589(1995).

FUNCTION: FACILITATIVE GLUCOSE TRANSPORTER. THIS ISOFORM MAY BE RESPONSIBLE FOR CONSTITUTIVE OR BASAL GLUCOSE UPTAKE. HAS A VERY BROAD SUBSTRATE SPECIFICITY; CAN TRANSPORT A WIDE RANGE OF ALDOSES INCLUDING BOTH PENTOSES AND HEXOSES (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PS00216; SUGAR_TRANSPORT_1; 1. PS00217; SUGAR_TRANSPORT_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             family
     Sugar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=8589457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUGAR_TRANSPORT_2; 1.
gar transport; Transport; Glycoprotein;
                                                                                                                                                                                                                   5 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

6 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

7 (POTENTIAL).
                                                                                                                          EXTRACELLULAR (POTENTIAL)
8 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
9 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL).
2 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
3 (POTENTIAL).
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1 (POTENTIAL).
                            CYTOPLASMIC
11 (POTENTIA
                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL) 4 (POTENTIAL).
     EXTRACELLULAR (POTENTIAL)
                                                                                                   EXTRACELLULAR (POTENTIAL)
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                                                                               (POTENTIAL)
                              (POTENTIAL
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Best Local
     DOMAIN
                                 TRANSMEM
                                                            DOMAIN
                                                                                     TRANSMEM:
                                                                                                        Repeat; Transmembrane;
                                                                                                                                                               PROSITE;
                                                                                                                                                                                                              Pfam; PF00083; sugar_tr; 1.
PRINTS; PR00171; SUGRTRNSPORT
                                                                                                                                                                                                                                                                                                                  EMBL; AF051139; AAC63975.1; -. EMBL; Z81312; CAB03595.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Connor R., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.; Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: HIGH-AFFINITY GLUCONATE TRANSPORTER.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales; Schizosaccharomyce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
High-affinity gluconate transporter ght3 (Hexose transporter 3).
GHT3 OR SPACIF8.01.
                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Heiland S., Radovanovic N., Hoefer M., Winderickx J., Lichtenberg "Multiple hexose transporters of Schizosaccharomyces pombe."; J. Bacteriol. 182:2153-2162(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GHT3_SCHPO
Q92339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20200352; PubMed=10735857;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SCHPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              194 VARTNGIKNAEETLNIEVVRSTMQEELDAAQTKTTVCDLFRNPSMRKRICILVFLR 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               135 WDLVCDYQSLKSVVQFLLLTGMLVGGIIGGHVSDRWLVESARWLIIT-NKLDEGLKALRK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             230 LRGTTDVSSDLQEMK-EESRQMMREK-----KVTIMELFRSPMYRQPILIAIVLQ 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
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                                                                                                                                                    PS00216; SUGAR_TRANSPORT_1; 1.
PS00217; SUGAR_TRANSPORT_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                          IPR003662; sub_transporter.
                                                                                                                                                                                                                                                                                   IPR003663; Sugar_transporter.
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450
177
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        9
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58
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87
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490
179
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                Sugar transport; Transport; Glycoprotein.
CYTOPLASNIC (POTENTIAL).
1 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
2 (POTENTIAL).
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CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 82.5; D
Pred. No. 7.7;
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N-LINKED (GL
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CYTOPLASMIC (POTENTIAL)
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(POTENTIAL)
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                                                                 142 QSLKSVVQFLLLTGMLVGGIIGGHVSDRWLVESARWLIITNKLDEGLKALRKVARTNGIK 201
                                                                                                                                                                                                                                                                                                                                    NIAMOC
230 EIIQT-NFNTIKSDI--EIEMAGGKARWIEIF-GKDIRYRTCLGFLVMLFREL 278
                   202 NAEETLNIEVVRSTMQEELDAAQTKTTVCDLFRNPSMRKRICI--LVFLRKKI 252
                                                185 NMLWGI---LLMVGVL-----
                                                                                         137 EVAPPQIRGAVVATYQ-----IFSTGAALVAACINMGTHKLRKTAS-----WRTSFGI 184
                                                                                                               82 NLRPEKCRRFVHPQWQLLHLNGTIHSTSEADTEPCVDGWVYDQSYFPSTIVTKWDLVCDY 141
                                                                                                                                       95 VYIIAELLLV-----TAVPS---WIQVLVGKILAGVGIGALSV-----LSPGYQS 136
                                                                                                                                                              22 VFILPSLMLLIPHILLENFAAAIPGHRCWVHMLDNNTGSGNETGILSEDALLRISIPLDS 81
                                                                                                                                                                                                    Similarity
                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     166
                                                                                                                                                                                                                                                                                                                                                                                                                                                            88
109
113
134
145
                                                                                                                                                                                                                                                  AA;
                                                                                                                                                                                                  5.9%;
22.3%;
                                                                                                                                                                                                                                                  62094 MW;
                                                                                                                                                                                        39; Mismatches
                                                                                                                                                                                                  Score 82.5; D
Pred. No. 8.9;
                                                                                                                                                                                                                                                N-LINKED (GLCNAC. . .) (: 30DFF04294D318DB CRC64
                                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                       SER-RICH.
                                                                                                                                                                                                                                                                                            11 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
12 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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7 (POTENTIA
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5 (POTENTIAL
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EXTRACELLULAR (POTENTIAL).
4 (POTENTIAL).
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                                            -FLPESPRYLIYKGRDEEALRIMCNMAELSPES
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                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                       91; Indels
                                                                                                                                                                                                            Length 555;
                                                                                                                                                                                                                                                           (POTENTIAL).
                                                                                                                                                                                      51;
                                                                                                                                                                                   Gaps
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Search completed: July 1, 2002, 11:43:04 Job time: 214 sec

## us-09-674-235-1.rpr

197.5 14.0 576 2 JR2509 193.5 13.8 557 2 JW0089 193.5 12.1 557 2 JW0089 169.5 12.1 593 2 JC4884 162.5 11.6 593 2 T27870 1 108 7.7 539 2 C96758 1 108 7.7 539 2 C96758 1 103 7.3 745 2 A31318 1 103 7.3 745 2 A31318 1 103 7.3 745 2 A31318 1 103 7.3 546 2 F69587 1 109 7.1 447 2 D89646 1 100 7.1 447 2 D89646 1 100 7.1 527 2 D	Description hypothetical pr	pred. No. is the number of results prediction from the score of the result being prince, score greater than or equal to the score distribution.  score greater than or equal to the score distribution.  score greater than or equal to the score distribution.  score greater than or equal to the score distribution.  score greater than or equal to the score distribution.	Database: pir_71:* 1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:* 4: pir4:*	Minimum DB seq length: 000000000000000000000000000000000000		/GGLGRFQMLH	OM protein - protein search, using sw model  (without alignments)  (without alignments)  (without alignments)  (without alignments)  (without alignments)  (without alignments)	GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.	Tue Jul 2 10:13:42 2002
Db  17 FDFVLEQVGNYGTYQIVFFFICLPTSLPSAFSAFNIP	JUETY MILES 90; INCEPT 19.08; FACE MISMATCHES 90; INCEPT 19.08; FACE MISMATCHES 90; INCEPT 19.08; MISMATCHES 90; MISMATC	tion: 1 16/1; 23/3; 50/1; 80/3; 108/2; 134/3; 227/7, 16/1; 23/3; 50/1; 80/3; 108/2; 134/3; 227/7, 14.0%; Score 197.5; DB 2; Length	e type: DNA s: 1-576 <wil> references: EMBL:283228; PT references: Clone F52F12 rental source: Clone F52F12.1 resp:F52F12.1</wil>	<b>G</b>	RESULT 1 T22509 hypothetical protein F52F12.1 - Caenorhabditis elegans hypothetical protein F52F12.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans	80 5.7 492 2	81 5.8 1737 2 T17101 81 5.8 2 E70732 proline-trun 80.5 5.7 260 2 H84198 hypothetical 80.5 5.7 515 2 B96825 cholesterol cholesterol C54E 80.5 5.7 512 2 A25922 protein C54E 80.5 5.7 583 2 F88642 MAPK-activat 80.5 5.7 359 2 JC4297 glucose tran	5.8 537 2 A79832 hypothetical 5.8 306 2 479832 cholesterol: 5.8 608 2 569564 cholesterol: 5.8 520 1 S03188 hypothetical 5.8 520 2 S04068 probable vol	conserved hyp 83 5.9 818 2 H82165 high-affinity 82.5 5.9 555 2 T38108 glucose trans 82.5 5.8 492 2 A27217 acrosomal pro

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A;Cross-references: DDBJ:AB017260; NID:g3869208; PIDN:BAA34399.1; PID:g3869209
                                                                                                                  C;Accession: JE0346

R;Sekine, T; Kusuhara, H.; Utsunomiya-Tate, N.; Tsuda, M.; Sugiyama, Y.; Kanai, Y.; End A;Title: Molecular cloning and characterization of high-affinity carnitine transporter facession: JE0346; MUID:99011422
                                                                                                             A; Molecule type: mRNA
A; Residues: 1-557 <SEK>
                                                                                                                                                                                                     high-affinity carntine transporter, CT1 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                            RESULT
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A;Experimental source: placenta
C;Comment: This transporter functions in the elimination of cationic drugs and other xen
                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-557 <WUA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 22.0%; Pred. No. 3.5e-09;
Matches 83; Conservative 37; Mismatches 106; Indels 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: cDNA sequence, transport function
A;Reference number: JW0089; MUID:98289574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C:Species: Homo sapiens (man)
C:Date: 18 Jun-1998 #sequence_revision 10-Jul-1998 #text_change 28-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Organic cation transporter protein 2 - human N.Alternate names: OCTN2
                                                                                                                                                                                                                                                                                                                                      339 NIRMVTIMSIMLWMTIS 355
                                                                                                                                                                                                                                                                                                                                                                  237 SMRKRICILVFLRKKIS 253
                                                                                                                                                                                                                                                                                                                                                                                             289 RFEEAEVIIRKAAKANGI----
                                                                                                                                                                                                                                                                                                                                                                                                183 KLDEGLKALRKVARTNGIKNAEETLNIEVVRST-----MQEELDAAQTKTTVCDLERNP 236
                                                                                                                                                                                                                                                                                                                                                                                                                            229 IFSTLGVCIFYAFGYMVLPLFAYFIRDWRMLLVALTMPGVLCVALMWFIPESPRWLISQG 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                       170 ----WLV-ESARWLITN 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 169 RKNVLFVTMGHQTGFSFLQIFSKNFEMFVVLFVLVGMGQISNYVAAFVLGTEILGKSVRI 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 170 ----- 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 EGESCLDGWEFSODVYLSTIVTEWNLVCEDDWKAPLTISLFFVGVLLGSFISGOLSDRFG 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    112 DTEPCVDGWVYDQSYFPSTIVTKWDLVCDYQSLKSVVQFLLLTGMLVGGIIGGHVSDR-- 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 AWRNHT------VPLRLRDGREVPHSCRRYRLATIANESALGLEPGRDVDLGQL 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 GSGNETGILSEDALLRISIPL---DSNLRPEKCRRF---VHPOWQLLHLN-GTIHSTSEA 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 YDEVTAFLGEWGPFÓ--RLIFFÚLSAS-IIPNGFTGLSSVFLIATPEHRCRVPDAANLSS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X.; Prasad, P.D.; Leibach, F.H.; Ganapathy, V. em. Biophys. Res. Commun. 246, 589-595, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 FEELLSQVGGLGRFQMLHLVFILDSLMLLIPH---ILLENFAAAIPGHRCWVHMLDN-NT 58
                                   13.78;
                      Score 193; DB 2;
Pred. No. 3.9e-09;
                                                                                                                                                                                                                                                                                                                                                                     -----VVPSTIFDPSELQDLSSKKQQSHNILDLLRTW 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         function, and genomic organization of human OCTN2, a
                            Length 557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12;
В
                        δδ
                                                      Дb
                                                                                γQ
                                                                                                             Б
                                                                                                                                       Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
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                                                                                                                                                               77;
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F:154-17/Domain: transmembrane #status predicted <TM2>
F:154-17/Domain: transmembrane #status predicted <TM2>
F:243-260/Domain: transmembrane #status predicted <TM3>
F:267-283/Domain: transmembrane #status predicted <TM4>
F:267-283/Domain: transmembrane #status predicted <TM4>
F:360-366/Domain: transmembrane #status predicted <TM5>
F:406-425/Domain: transmembrane #status predicted <TM5>
F:406-425/Domain: transmembrane #status predicted <TM6>
F:469-485/Domain: transmembrane #status predicted <TM9>
F:469-485/Domain: transmembrane #status predicted <TM9>
F:469-485/Domain: transmembrane #status predicted <TM10>
F:495-452/Domain: transmembrane #status predicted <TM10>
F:494-514/Domain: transmembrane #status predicted <TM10>
F:494-514/Domain: transmembrane #status predicted <TM10>
F:71,97,113,432/Binding site: carbohydrate (Asn) (covalent) #status predicted 
F:286,292/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted 
F:296,343,550/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted 
F:296,343,550/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted 
F:296,343,550/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted (Thr) (covalent) (covalent) (by protein kinase C) #status predicted (Thr) (covalent) (covalent) (covalent) (covalent) 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-342,'N', 344-556 <GOR>
A; Cross-references: EMBL: X78855, NID: 9633621; PIDN: CAA55411.1; PID: 9633622
C; Keywords: 91 ycoprotein; phosphoprotein; transmembrane protein
F; 20-46/Domain; transmembrane #status predicted <TMI>
F; 20-46/Domain; transmembrane #status predicted <TMI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library, January 1995
A;Reference number: S78533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: kidney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organic cation transport protein OCT1 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 05-Nov-1999
C;Accession: S50862; S78533; I58089
R;Gruendemann, D.; Gorbboulev, V.; Gambaryan, S.; Veyhl, M.; Koepsell, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-556 <GRU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Reference number: I58089; MUID:95082907

A:Molecular S50862
109 SIVANRSQLPLGPCEHGWVYDTP--GSSTVTEFNLVCGDAWKVDLFQSCVNLGFFLGSLV 166
                                                            103 GTIHSTSEADTEPCVDGWVYDQSYFPSTIVTKWDLVCDYQSLKSVVQFLLLTGMLVGGII 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cross-references: EMBL:X78855; NID:g633621; PIDN:CAA55411.1; PID:g633622
                                                                                                                            62 CGWSQAEELNYTVPGLGPSDEASFLSQ--CMRYEV--DWNQSTLDC----VDP-----LS 108
                                                                                                                                                                                        50 --WVHMLDNN-----TGSGNETGILSEDALLRISIPLDSNLRPEKCRRFVHPOWOLLHLN 102
                                                                                                                                                                                                                                                                                                                    4 EELLSQVGGLGREQ---MLHLVFILPSLMLLIPHILLENFAAAIPGHRC------ 49
                                                                                                                                                                                                                                                        5 DDVLEQVGEFGWFQKQAFLLLCLISASLAPIYVGIVFLGFT---PGHYCQNPGVAELSQR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    166 REGRKNY--LELIMGMQTGESELQ 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             169 RWLVESARWLIITNKLDEGLKALR 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               106 EQLEQENCLDGWEYNKDVFLSTIVTEWDLVCKDDWKAPLTTSLFFVGVLMGSFISGQLSD 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109 SEADTEPCVDGWVYDQSYFPSTIVTKWDLVCDYQSLKSVVQFLLLTGMLVGGIIGGHVSD 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58 LSSAWRNH-----SIPLETKDGRQVPQSCRRYRLATIANFSALGLEPGRDVDL 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56 NNTGSGNETGILSEDALLRISIPL---DSNLRPEKCRRP---VHPQWQLLHLN-GTIHST 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 YDEVTAFLGEWGPFO--RLIFFILSAS-IIPNGENGMSIV---FLAGTPEHRCLVPHTVN 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 FEELLSOVGGLGREOMLHLVFILDSLMLLIPH-----ILLENFAAAIPGHRCWV-HMLD 55
                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63; Conservative
                                                                                                                                                                                                                                                                                                                                                        12.1%; Score 169.5; DB 2; Leny... 20.5%; Pred. No. 4.7e-07; Mismatches 95; Indels 157; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                    15;
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organic cation transporter protein 2 - rat c;Species: Rattus norvegicus (Norway rat) c;Species: Rattus norvegicus (Norway rat) c;Date: 10-Sep-1996 #sequence_revision 18-Oct-1996 #text_change 05-Nov-1999 c;Accession: JC4884 R;Okuda, M.; Saito, H.; Urakami, Y.; Takano, M.; Inui, K. Biochem. Biophys. Res. Commun. 224, 500-507, 1996 A;Title: cDNA cloning and functional expression of a novel rat kidney organic cation tra A;Reference number: JC4884; MUID:96295517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: DDBJ:D83044; NID:91502282; PIDN:BAA11754.1; PID:d1012421; PID:91502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-593 <OKU>
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hypothetical protein ZK455.8 - Caenorhabditis elegans C;Species: Caenorhabditis elegans
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          175 ARWLIITNKLDEGLKALRKVARTNG-IKNAEETLNIEVVRSTMQEELDAAQTKT-TVCDL 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               167 VGYIADRFGRKLCLLVTTLVTSVSGVLTAVAPDYTSMLLFRLLQGMVSKGSWVSGYTLIT 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  233 FRNPSMRKRICILVFL 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     227 EFVGSGYRRTTAILYQMAFTVGLVGLAGVAYAIPDWRWLQLAVSLPTFLFLLYYWFVPES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            163 GGHVSDR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                     164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  110
                                                                                                                                  342 PQIRKHTLILMY 353
                                                                                                                                                                                                                            288
                                                                                                                                                                                                                                                                                                                   228 FYGLGYRRMYGICYQIAFTYGLLILAGVAYYIPNWRWLQFAYTLPNFCFLLYFWCIPESP
                                                                                                                                                                                                                                                                                                                                                                                                             168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104 TIHSTSEADTEPCVDGWVYDQSYFPSTIVTKWDLVCDYQSLKSVVQFLLLTGMLVGGIIG 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRTPTLRKHTVILMYL 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                     GHVSDR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GWSQAEELNYTVPGLGPSDEASFLSQ--CMRYEV--DWNQSTLDC---VDP-----LSS 109
                                                                                                                                                                               PSMRKRICILVF 247
                                                                                                                                                                                                                         RWLISQNKIVKAMKIIKHIAKKNG-----KSVPVSLQNLTPDEDA-GKKLKPSILDLVRT 341
                                                                                                                                                                                                                                                                      RWLIITNKLDEGLKALRKVARTNGIKNAEETLNIEVVRSTMQEELDAAQTKTTVCDLFRN 235
                                                                                                                                                                                                                                                                                                                                                                                                        GYLADRFGRKFCLLVTILINAISGALMAISPNYAWMLVFRFLQGLVSKAGWLIGYILITE 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAADRNQLPLGPCEHGWVYNTP--GSSIVTEFNLVCAHSWMLDLFQSVVNVGFFIGAMMI 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DDILEHIGEFHLFQ--KQTFFLLALLSGAFTPIYVGIVFLGFTPDHHCWSPGAAKLSQRC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EELLSQVGGLGRFQMLHLVFILPSLM--LLIPHILLENFAAAIPGHRCW-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------VHMLDNNTGSGNETGILSEDALLRISIPLDSNLRPEKCRREVHPQWQLLHLNG 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 162.5; DB 2; Pred. No. 2.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------ 172
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                                                                                                                                                                                                                                                                                                                                                                -----ESA 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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submitted to the EMBL Data Library, November 1995 A; Reference number: Z20432 A; Accession: T27870
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QΥ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:266567; PIDN:CAA91492.2; GSPDB:GN00028; CESP:ZK455.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-794 <WIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: CESP: ZK455.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Experimental source: clone ZK455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
A; Map position: V
A; Introns: 12/2; (
A; Note: T08B1.1
                                                                                                                                                                                                                          R;Henkhaus, J.; Wohldmann, P.; Leimbach, D. submitted to the EMBL Data Library, August 1999 A;Description: The sequence of C. elegans cosmid T08B1 A;Reference number: Z20926
                                                                                                                                                                                                                                                                                                                sugar transport protein homolog T08B1.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 29-Oct-1999
C;Accession: T30895
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                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-591 <HEN>
                                                                    C; Genetics:
                                                                                       A; Experimental source: strain Bristol N2
                                                                                                               A;Cross-references: EMBL:AF039039; PIDN:AAB94177.2
                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                271 VKDMNATGKINRCKE------WEYDTSVMDRTIVTEWNRVCDNNWSRAHVHMSYSLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          442 LYFLPESPRWLILNNKTKQAEKIIREACHYN---KSRLPSDLGLVRHAEKKKWMKHNEKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  171 ---LVESARWLIITNKLDEGLKALRKVARTNGIKNAEETLNIEVVRSTMQEELDAAQTKT 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       156 MLVGGIIGGHVSDRW------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          212 NEESFSA-ELGYTNYTWDQVLNSTIAFPRTFNKQRNELHHDQCHYFERDYVHIKLSPWAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  156 FEEDDLGILQLIGGCSYWQI--IVYLIISVQ-QVPHAMF-NLSVVYMMYQPDHWCKIPFF 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    499 SYFHLFRSSELRFRNVVL 516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLHLN--GTIHSTSEADTEPCVDGWVYDQSYFPSTIVTKWDLVCDYQSLKSVVQFLLLTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAYVLCMEVTGTKYRSIVGSLIQAPWACGYAFLALIAYLTKSWTMIHLICVLLHIISLML 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNNTGSGNETGILSE--DALLR--ISIPLDSN-----LRPEKC----RREVH----PQWQ 97
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                          62/1; 89/1; 111/3; 145/3; 325/2; 359/1; 468/2; 540/2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 156; DB 2;
Pred. No. 1.1e-05;
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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Attle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
A;Rocession: C96758
A;Status: preliminary A;Residues: 1-539 <STO>
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A; Gene: T18K17.11
A; Map position: 1
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar_2001 *sequence_revision 02-Mar-2001 *text_change 31-Mar-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 7.5%; Score 106; DB Best Local Similarity 15.4%; Pred. No. 0.19;
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ζ
                                      172
                                                                171 SCVLTFVTAFAISFSPNVWVYAFLRFANGFFRSGIGSCCIVLATEIVGKKWRGQVGQYGF 230
                                                                                                                                                                                       120 WYYDQSYFPSTIVTKWDLVCDYQSLKSVVQFLLLTGMLVGGIIGGHVSDRWL----- 171
                                                                                                                                                                                                                                                                                    60
                                                                                                                                                                                                                                                                                                                   43 LTVDEVIEQHIGALGFAQILHALLVSIAWIFDAQTTLISIFSDAQPAARLLA------
                                                                                                                                                                                                                                                                                                                                                       1 MAFEELLSQ-VGGLGRFQMLHLVFILPSLMLLIPHILLENFAAAIPGHRCWVHMLDNNTG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77
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                                                                                                                                                   WIGPKS---DTVVSEWNLICQHKFLVAVPSTLFFIGSLFGSGVYGYLADSWFGRKKTLLL 170
                                                                                                                                                                                                                                                                       SGNETGILSEDALLRISIPLDSNLRPEKCRRFVHPQWQLLHLNGTIHSTSEADTEPCVDG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DTEPCVDGWVYDQSYFPSTIVTKWDLVCDYQSLKSVVQFLLLTGMLVGGIIGGHVSDRW- 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -NNTGSGNETGIL---SEDALLRISIPLDSNLRPEKCRRFVHPQWQLLHLNGTIHSTSEA 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VIMVNAFQWPIAYMTIALIAWL 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTVCDLFRNPSMRKRICILVFL 248
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45; Mismatches
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                            -VESARWLIITNKLDEGL 188
                                                                                                                                                                                                                                                                                                                                                                                                     Indels 164;
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          R;Fukumoto, H.; Seino, S.; Imura, H.; Seino, Y.; Eddy, R.L.; Fukushima, Y.; Byers, M. Proc. Natl. Acad. Sci. U.S.A. 85, 5434-5438, 1988
A;Title: Sequence, tissue distribution, and chromosomal localization of mRNA encoding A;Reference number: A31318; MUID:88289735
                                                                                                                               glucose transporter-like protein - human
C;Species: Homo sapiens (man)
C;Date: 28-Feb_1990 #sequence_revision 28-Feb-1990 #text_change 24-Sep-1999
    A; Molecule type: mRNA
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A; Residues: 1-745 <WOH>
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72; Conserv
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hypothetical protein K05F1.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T16565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Introns: 70/2; 160/3; 205/3; 249/3; 293/2; 350/1; 386/3; 462/3; 546/2; 669/3; 680/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:U29377; NID:9868173; PID:9868176; PIDN:AAA68713.1; CESP:K05FA;Experimental source: strain Bristol N2
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                                                                216 MQEELDAAQTKTTVCDLFRNPSMRKR---ICILVFL 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            165 ---NDT----NDTTISSHGPYLWGVDDIKNISFVFPNANSDGAYQRDSCYFYERSEERYRQ 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113 FEGILNIIGGCRWWQI--WIYVLIALQ-QIPHAMFNLNVVYMMYDPEFQCMVPGF----- 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53 MLDNNTGSGNETGILSE-----DALLRISIPL-----DSNLRPEKCRRFVHPQWQLLH 100
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KLNKKNGG--KIGFLDLFTMKELRYRTISVCI-VFM 490
                                                                                                                                 IFICSIPESPRWLMVQNRVSEAEEVIRKACREPPFPFNMCTTSKCGNLPSDLELVSHRER 457
                                                                                                                                                                                                                                                                  DLAAYTLCMEITGTKYRAMVGSMLQAPWALGYALLALIAYLTKSWKTIQVIAAGLHFMSI 397
                                                                                                                                                                                                                                                                                                                                                                                                   IGYLLGCVLGGIASDKIGRKPTIIGFGILSSMLGVFLPFNDYYPMFLLIRLLSAICNEAA 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGMLVGGIIGGHVSDR------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LRRMPLETAMSEAWKDVAPKKKC-QAYHFEKDVMVETIVTDFNLVCDSWFAKGHAHMFYS 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LN----GTIHSTSEADTEP----CVDGWVYDQSYFPSTIVTKWDLVCDYQSLKSVVQFLLL 153
                                                                                                                                                                                                 -----LVESARWLIITNKLDEGLKALRKVAR------TNGIKNAEETLNIEVVRST 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.3%;
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Pred. No. 0.53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----- 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     112; Indels 168;
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A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_elegans/ ac.uk/Projects/C_elegans/ ac.uk/Projects/ ac.uk/Projects/C_elegans/ ac.uk/Projects/ ac.uk/Projec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: ZK455.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Note: Similarity to sugar transporters
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-447 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein ZK455.8 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;anonymous, The C. elegans Sequencing Consortium. Science 282, 2012-2018, 1998
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A;Cross-references: GB:J03810; NID:g187133; PIDN:AAA59514.1; PID:g307125 C;Genetics: A;Gene: GDB:SLC2A2; GLUT2 A;Cross-references: GDB:I19995; OMIM:138160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C:Accession: D89646
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C:Superfamily: glucose transport protein
C:Keywords: transmembrane protein
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                                                                                             181 KSRLPSDLGLVRHAEKKKWMKHNEKPSYFHLFRSSELRFRNVVL 224
                                                                                                                                                                             202 NAEETLNIEVVRSTMQEELDAAQTKTTVCDLFRNPSMRKRICIL 245
                                                                                                                                                                                                                                                             124 LIAYLTKSWTMIHLICVLLHIISLMLLYFLPESPRWLILNNKTKQAEKIIREACHYN--- 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 TIVTKWDLVCDYQSLKSVVQFLLLTGMLVGGIIGGHVSDRW-------
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                                                                                                                                                                                                                                                                                                                                                                                                                              64 LTYSKEFEIFLVVRFLLAATNEAADLAAYVLCMEVTGTKYRSIVGSLIQAPWACGYAFLA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         304 ILVALML 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              250 LDEEVKAKQSLKRLRGYDDVTKDIN-----EMRKEREEASSEQKVSIIQLFTNSSYRQP 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184 LDEGLKALRKVARTNGIKNAEETLNIEVVRSTMQEELDAA--QTKTTVCDLFRNPSMRKR 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           149 OFLLLTGMLVGGIIG-----GHVSDRWLV--------ESARWLIITNK 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 ICILVFL 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 TIVTEWNRVCDNNWSRAHVHMSYSLGYLVGCFVGGFISDRYGRKTAITGEGILTMLEGFL 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            h 7.0%; Score 98.5; DB 2; Length 447; Similarity 17.4%; Pred. No. 0.71; 39; Conservative 22; Mismatches 52; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.18; 27.68;
                                                                                                                                                                                                                                                                                                                                                  ------LVESARWLIITNKLDEGLKALRKVARTNGIK 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34; Indels
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L-arabinose transport (permease) araE - Bacillus subtilis
C;Beccies: Bacillus subtilis
C;Dete: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C;Accession: F69587
C;Accession: F69587
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber
C; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
R; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino
A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete
A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se
A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasunoto, K.; Yasanoto, V.; Uchlya-
A; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili
A; Accession: F69587
A; Status. prolimicary. Park (19844033)
A. Molecule type: mRNA
A. Molecule type: mRNA
A. Molecule type: mRNA
A. Molecule type: mRNA
A. Residues: 1-105, 'D',107-180, 'T',182-326, 'T',328-350, 'F',352-431, 'P',433-523 <ASA>
A. Cross-references: EMBL:X15684; NID:g51090; PIDN:CAA33719, 1; PID:g51091
R. Hogan, A.; Heyner, S.; Charron, M.J.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.;
Development 113, 363-372, 1991
                                                                                                                                                                                                                                                       A;Cross-references: EMBL:X16986; NID:g55511; PIDN:CAA34855.1; PID:g55512 R;Asano, T.; Shibasaki, Y.; Lin, J.L.; Akanuma, Y.; Takaku, F.; Oka, Y. Nucleic Acids Res. 17, 6386, 1989
A;Title: The nucleotide sequence of cDNA for a mouse liver-type glucose transporter p A;Reference number: S05319; MUID:89366666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C:Species: Mus musculus (house mouse)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 24-Sep-1999
C:Accession: S06920; S05319; B444887; 148367
R:Suzue, K.; Lodish, H.F.; Thorens, B.
Nucleic Acids Res. 17, 10099, 1989
A:Title: Sequence of the mouse liver glucose transporter.
A:Reference number: S06920; MUID:90098776
                                                                                                                                                                                                                                               A; Accession: S05319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-523 <SUZ>
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A;Experimental source: strain 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  133 TKWDLVCDYQSLKSVVQFLLLTGMLVGGTIGGHVSDRWLVESARWLIITNKLDEGLKALR 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184 TGWRWMLAYGMVPSVIFFLVL---LV-----
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A; Note: sequence extracted from NCBI backbone (NCBIN:77926, NCBIP:77927)
R; Waeber, G.; Thompson, N.; Haefliger, J.A.; Nicod, P.
JBiol. Chem. 269, 26912-26919, 1994
A; Title: Characterization of the murine high Km glucose transporter GLUT2 gene and its A; Reference number: A55078; MUID:95014557
A; Accession: I48367
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-5 < RES>
A; Residues: 1-5 < RES>
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A;Residues: 384-431,'p',433-496 <HOG>
A;Cross-references: GB:577926; NID:g242129; PIDN:AAB20847.1; PID:g242130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Glucose transporter gene expression in early mouse embryos. A;Reference number: A44887; MUID:92111400 A;Accession: B44887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: GLUT2
C;Superfamily: glucose transport protein
C;Keywords: liver; transmembrane protein
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Vature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable membrane transporter [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001 C;Accession: G84864 R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Faring, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Faring, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Faring, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Faring, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Faring, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Faring, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Faring, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Faring, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Faring, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Faring, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Faring, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Faring, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Faring, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Faring, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Faring, X.; Kaul, S.; Kaul,
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A; Residues: 1-521 <STO>
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G84864
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C; Superfamily: glucose transport protein
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            178 LIITNKLDEGLKALRKVARTNGIKNAEETLNIEVVRSTMQEELDAAQT--KTTVCDLFRN 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  186 ALGTLHQLALVTGILISQIAGLSFILGN-QDHWHILLGLSAVPALLQCLLLLFCPESPRY 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        143 SLKSVVQFLLLTGMLVGGIIG-----GHVSDRWLV------ESARW 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    297 ANYROPILVALML 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     236 PSMRKRICILVFL 248
                                               181 TNKLDEGLKALRKVARTNGIKNAEETLNIEVVRSTMQEELDAAQTKTTV--CDLFRNPSM 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 6.8%;
Local Similarity 25.6%;
                                                                                                                                          188 SYLVNSAFTQVPGTWRWMLGVSGVPAVIQFILML---
                                                                                                                                                                                                                           125 SYFPSTIVTK----WDLVCDYQSLKSVVQFLLLTGMLVGGIIGGHVSDRWLVESARWLII 180
                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                      6.6%; Score 93; DB: 26.9%; Pred. No. 2.6; ative 23; Mismatches
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                                                                                                                                                             ----FMPESPRWLFM 232
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Job time: 248 sec

Search completed: July 1, 2002, 11:41:47

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A;Cross-references: GB:J03145; NID:g204534; PIDN:AAA41298.1; PID:g204535 R;Ahn, Y.; Kim, G.; Lee, B.; Kim, Y. Arch. Biochem. Biophys. 323, 387-396, 1995 A;Title: Cloning and characterization of rat pancreatic beta-cell/liver type glucose A;Reference number: S68362; MUID:98063615 A;Accession: S68362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    glucose transport protein, hepatic - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 17-Nov-2000
C;Accession: A31556; S68362
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                                                                                                                                                                                                                                                                                                                                                                                                                           C;Genetics:
A;Introns: 5/3; 36/3; 122/2; 164/1; 202/3; 257/1; 319/3; 354/3; 388/3; 456/3
C;Superfamily: glucose transport protein
C;Keywords: liver; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-246, 'K', 248-522 <AHN>
A; Cross-references: EMBL: L28134
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A; Residues: 1-522 <THO>
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                                                                                                                                              178 LIITNKLDEGLKALRKVARTNGIKNAEETLNIEVVRSTMQEELDAAQT--KTTVCDLFRN 235
                                                                                                                                                                                                 185 ALGTLHQLALVTGILISQIAGLSFILGN-QDYWHILLGLSAVPALLQCLLLLLFCPESPRY 243
                                                                                                                                                                                                                                         143 SLKSVVQFLLLTGMLVGGTIG-----GHVSDRWLV------ESARW 177
                                                                                                244 LYL--NLEEEVRAKKSLKRLRGTEDITKDIN-----EMRKEKEEASTEQKVSVIQLFTD 295
296 PNYRQPIVVALML 308
                                                   236 PSMRKRICILVFL 248
                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                       33;
                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                               6.6%; Score 93; DB 24.8%; Pred. No. 2.6;
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Database
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Maximum Match 10
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Maximum DB seq length: 200000000
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112:
12:
14:
7: //SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/Na1986.DAT: *
8: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/Na1987.DAT: *
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23: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/Na20011.DAT: *
23: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/Na20011.DAT: *
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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993 - 2000 Comp
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/SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1985.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

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SUMMARIES	
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9	8	7	6	U	4	ω	N	-	Result
314.2	332	335.2	335.2	508	508	782	804	804	Score
39.1	41.3	41.7	41.7	63.2	63.2	97.3	100.0	100.0	% Query Match
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AAC85823	AAC61892	AAD09561	AAI59215	AAC85824	ABA08976	AAH98847	AAZ38317	AAZ38316	ID
hOAT4 DNA. Homo s	cDNA encoding a hu	Human transporter	Human polynucleoti	hOAT5 DNA. Homo s	Human secreted pro	<ul> <li>Human EST-derived</li> </ul>		Human transmembran	Description

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## ALIGNMENTS

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RESULT
AAZ38316
ID AAZ3
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KW Orga
KW Or
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                                                                                                     28-APR-1998;
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     (SAGA ) SAGAMI CHEM RES CENT
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/note= "No stop codon given in the specification"
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Matches 804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents the coding sequence of human cDNA clone HP02000 which encodes a 32 kD protein with two putative transmembrane domains. The cDNA was isolated from a human liver cell cDNA library, and from tissue localisation studies has been found to be expressed only in the liver. The protein has homology with the rat organic cation transporter (EMBL Accession No. V09945) which is involved in drug excretion, and may have a similar function. The protein may be used to raise specific antibodies, as assay reagents, as diagnostic tissue markers, for the isolation of cognate receptors, ligands and binding proteins, and as biologically active agents. Nucleotides encoding the protein may be used as primers and probes or antisense molecules, and in gene therapy. Cells transformed with these nucleotides may be used to screen for agonists and antagonists which are
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  ligands and binding proteins, and as biologically
                                                                                                                                                                                                                          Claim
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                                                                                                                                                                                                                                                                                                                                                                                                         Kato
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the liver. The protein has homology with the rat organic cation transporter (EMBL Accession No. 709945) which is involved in drug excretion, and may have a similar function. The protein may be used to raise specific antibodies, as assay reagents, as diagnostic tissue markers, for the isolation of cognate receptors,
                                                                                                                      domains. The cDNA was isolated from a human liver cell cDNA library, from tissue localisation studies has been found to be expressed only
                                                                                                                                                                  encodes a
                                                                                                                                                                                                                                                                                                         Human proteins with transmembrane proliferation and differentiation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-NOV-1999.
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DB; AAY52386.
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                                                                                                                                                                                                                                         Page 89-91; 114pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kimura
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03-AUG-2000;
15-SEP-2000;
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                                                                                                                                                                                                                                                                                                                       The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiinflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic; cytostatic; osteopathic; vasotropic; cardiant; virucide; antibact
                                                                         03-FEB-2000; 2000US-0496914.
27-APR-2000; 2000US-0560875.
                                                                                                                                                                                  05-FEB-2001; 2001WO-US03800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; cytokine; cell proliferation; cell differentiation; growth factor; haematopoiesis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder;
(HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                      antifungal; vulnerary; antiulcer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human secreted protein homologue-encoding cDNA, SEQ ID NO:752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABA08976 standard; cDNA; 1353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      virucide; antibacterial;
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CC haematopoiesis regulatory activity; tissue growth activity; cismunomodulatory activity; activity: haemostatic, thrombotic or chemokinetic activities; proliferation or metastasis.

CC pending on their biological activities, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include conditions, e.g., by protein or gene therapy. Such conditions include conditions, e.g., by protein or gene therapy. Such conditions or arthritis), cronic inflammatory conditions (e.g., asthma or arthritis), conditions include cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell conditions, chronic inflammatory conditions (e.g., asthma or arthritis), conditions bone disorders (e.g., osteoporosis) and abnormal consciular growth. Polypeptides involved with tissue regeneration and conceptation (e.g., of burns, incisions and ulcers), while those with conditions of the inflammatory activities may be used in the treatment of viral, conditions in addition to immune disorders.
                                                Polypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a cDNA encoding a novel human polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention in have various activities, including cytokine, cell proliferation or cell differentiation activities; stem cell growth factor activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides are polypeptides in a sample, and methods of identifying compounds which being the polypeptides in a sample, and methods of identifying compounds which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tang
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Pred. No. 6.2e-153;
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Sequence 1353 BP; 349 A; 298 C; 315 G; 391 T; 0 other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  membrane protein; transport; organic anion; splice variant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; organic anion transporter; hOAT; liver; kidney;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                          12-JUL-2000; 2000WO-US18980
                                                                                                                                                                                                                                                                                                                                                                                                                                       18-JAN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200104283-A2.
                                                                                                                                                                                                                                                                                                                                               (META-) METABASIS THERAPEUTICS INC.
                                       transporter (hOAT) polypeptides are preferentially transporter (hOAT) polypeptides are preferentially expressed in the liver and kidneys of humans. OAT's are membrane expressed in that facilitate the transport of organic anions across the proteins that facilitate the transport is thought to be a secondary cell membrane. The mechanism of transport is thought to be a secondary or tertiary active transport involving exchange of another organic anion. Or tertiary active transport involving exchange of another organic anion. Or tertiary active transport involving exchange of another organic anion. It is a secondary to be splice variants as they are how identical except at the C-terminal end. how proteins and the DNA identical except at the C-terminal end. how proteins and the DNA identical except at the C-terminal end.
                                                                                                                                                                                                                                                                                                                   Sun W;
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                                                                                                                                                                                            Claim 1; Fig 6; 95pp; English.
                                                                                                                                                                                                                          useful in gene therapy procedures -
                                                                                                                                                                                                                                        Nucleic acids encoding human organic anion transporter polypeptides,
                                                                                                                                                                                                                                                                      P-PSDB; AAB47276
                                                                                                                                                                 The sequences given in AAC85819-24 encode human organic anion
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                           diseases associated with inappropriate hOAT expression
                                                                                                                                                                                                                                                                                         2001-367057/38.
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                                                                                                                                                                                                                                                                                                                                                                                   99US-0143771.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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Sequence 2684 BP; 800 A; 533 C; 541 G; 810 T; 0 other;

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                                                                                                                                                                                                                                                                                                                                                                                          Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance) peripheral nervous system; neuropathy; central nervous system; CNS; peripheral nervous system; neuropathy; central nervous system; CNS; Alzhelmer's; parkinson's disease; Huntington's disease; haemostatic; anyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; anyotrophic thrombolytic; drug screening; arthritis; inflammation; chemokinetic; thrombolytic; drug screening;
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09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
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                                                                                                                                                         26-DEC-2000; 2000WO-US34263.
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25-APR-2000;
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     , 2000US-0488725.
; 2000US-0552317.
; 2000US-0598042.
; 2000US-0620312.
; 2000US-0653450.
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708 totcaatcacigacticagiggctaaattigtattcatggctggaatgatggtgggaggc
               421 tatcagtcactgaaatcagtggttcaattcctacttctgactggaatgctggtgggaggc 480
                                                          648 gtgtatgacagaatctccttctcatccaccatcgtgactgagtgggatctggtatgtgac 707
                                                                             361 gtatatgatcaaagctacttcccttcgaccattgtgactaagtgggacctggtatgtgat 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunosuppressant and cytostatic activity. The polypoptide or polypucleotides are useful in gene therapy. A composition containing a polypoptide or polypucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous localised neuropathies and central nervous system diseases, such as lateral sclerosis, and shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, and shy-Drager Syndrome. Other uses include the activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                              468 gacaatgacactggggccctcagccaagatgcactcttgagaatctccatcccactggac 527
                                                                                                                                                                                                                                                                                                                       121 gctgcagccattcctggtcatcgttgctgggtccacatgctggacaataatactggatct 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 1418; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
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19-OCT-2000; 2000US-0693036.
29-NOV-2000; 2000US-0727344.
                                                                                                                       ctgaatgggaccttccccaacaagtgacgcagacatggagccctgtgtgggatggctgg 647
                                                                                                                                         Local
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Zhou P,
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Wehrman T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41.7%; Score 335.2;
78.7%; Pred. No. 3e-
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Yang Y,
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                                                                                                                                                                                  Human; transporter and ion channel-10; TRICH-10; cystic fibrosis; mood; gene therapy; amyotrophic lateral sclerosis; amnesia; muscular dystrophy, hypertension; angina; neurological disorder; asthma; bipolar disorder; plck's depression; Alzheimer's disease; epilepsy; vaccine; arrhythmia; huntington's disease; hental disorder; schizophrenia; hold; anxiety; stroke; muscle disorder; cardiomyopathy; cataract; myocarditis; drave's disease; muscular disorder; schizophrenia; polymyositis; dermatomyositis; diabetes mellitus; immunological disorder; psoriasis; sickle cell anaemia; wilson's disease; infertility; Cushing's disease; sickle cell anaemia; wilson's disease; infertility; Cushing's disease; malabsorption syndrome; hypercholesterolaemia; cancer; ss.'
                                                                      WO200146258-A2.
                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                             Human transporter and ion channel-10 (TRICH-10) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-SEP-2001 (first entry)
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                                                                                      /product= "Human TRICH-10 protein"
                                                                                                                                        Location/Qualifiers
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P-PSDB; AAE04897. Baughn MR, Burford N, Hillman JL, Azimzai Y (INCY-) INCYTE GENOMICS INC. 14-JAN-2000; 21-JAN-2000; 28-JAN-2000; 23-DEC-1999; 22-DEC-2000; 2000WO-US35095 2001-418042/44. Khan FA; 2000US-0177332; 2000US-0178572; 2000US-0179758; 2000US-0181625; 99US-0172000. 2000US-0176083. Au-Young J, Lu DAM, Yue H, Nguyen DB, Yang J, Yao MG,

PR PR PR

Novel human transporter and ion channel proteins useful for treating and preventing transport, neurological, muscle and immunological

Claim 5; Page 147; 160pp; English.

PR XXX PR PI PA X XXX PR PI PA X disease, Duchenne muscular dystrophy, angina and hypertension, neurological disorders including Alzheimer's disease, amnesia, bipolar The present sequence is transporter and ion channel-10 (TRICH-10) cDNA. TRICH is used as vaccine. TRICH is useful for treating a disease or condition associated with decreased expression of functional TRICH, such as transport disorder including amyotrophic lateral sclerosis, cystic fibrosis, Becker's muscular dystrophy, Charcot-Marie Tooth disease Duchanne muscular dustronhy and humantaries. dementia, depression, epilepsy, ischaemic cerebrovascular

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osteoarthritis; burn; incision; ulcer; periodontal disease; neuropathy; nervous system disease; bone growth; cosmetic plastic surgery; gut protection; gut regeneration; fibrosis; cancer;
                                                              Secreted
                                                                                               cDNA encoding a human secreted protein.
                                                                                                                                         06-MAR-2001
                                                                                                                                                                                                                        AAC61892 standard;
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                                                        protein; platelet disorder; stem cell disorder; osteoporosis;
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                                                                                                                                                                                                                      cDNA;
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AAC61879-93 encode secreted human proteins. The secreted proteins are useful in assays to determine their biological activities. The proteins can also be used as biomarkers to identify tissues or cell types which express the proteins. The polynucleotide molecules can be used as biomarkers for tissues or chromosomes and to elicit immune responses. The proteins and antibodies are useful in diagnosis and treatment of diseases associated with altered expression of these proteins. The proteins are also useful for prevention or treatment of platelet disorders, stem cell disorders, osteoporosis or osteoarthritis, burns, inclisions, ulcers, periodontal diseases, central and peripheral nervous system diseases and neuropathies, for healing fractured bones and to induce cartilage and/or bone growth in cosmetic plastic surgery. The proteins are also useful for gut protection or regeneration, for the treatment of lung or liver fibrosis, for stimulating blood cell
                                   generation in patients receiving cancer chemotherapy and for treatment of bone marrow transplantation patients.
                                                                                                                                                                                                                                                                                                                                                                       Novel secreted human proteins useful for stimulating blood cell generation in patients receiving cancer chemotherapy, treating l marrow transplantation patients and for healing fractured bones
Sequence 2027 BP; 530 A; 501 C; 459 G; 537 T; 0 other;
                                                                                                                                                                                                                                                                                                                                           Claim 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDS
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20-AUG-1999;
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                                                                                                                     gctgcagccattcctggtcatcgttgctgggtccacatgctggacaataatactggatct
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                                           ggtaatgaaactggaatcctcagtgaagatgccctcttgagaatctctatcccactagac
                                                                                                                                                               actgtttttctctcaatctttgctgttgctacataccttcattttatgctggagaacttc
                                                                                                    actgcattcatacctggccatcgctgctgggtccacatcctggacaatgacactgtctct
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Pred. No. 4.1e-96;
0; Mismatches 110;
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                                                                                                        The sequences given in AAC85819-24 encode human organic anion transporter (hOAT) polypeptides. hoAT polypeptides are preferentially expressed in the liver and kidneys of humans. OAT's are membrane proteins that facilitate the transport of organic anions across the cell membrane. The mechanism of transport is thought to be a secondary or tertiary active transport involving exchange of another organic anion hOAT2A and hOAT2B are thought to be splice variants as they are identical except at the C-terminal end. hOAT proteins and the DNA identical except at the C-terminal end. hOAT proteins and the DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
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  Sequence 1977 BP;
                                                                                         encoding them, may be used in the prevention,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding human organic anion transporter polypeptides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-JUL-1999;
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                                                     diseases associated with inappropriate hOAT
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DB; AAB47275.
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in; transport; organic anion; splice variant;
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     502 A; 491 C;
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450 G;
     534 T; 0 other;
                                                                                         treatment and diagnosis
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09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
                                                                                                                                                                                                                                                     Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance peripheral nervous system; neuropathy; central nervous system; neuropathy; central nervous system; CNS; Alzheimer's; parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                                                                    21-JAN-2000;
25-APR-2000;
                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                           Human polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                              AAI61001 standard; cDNA;
                                                                                                               26-DEC-2000;
                                                                                                                                           26-JUL-2001
                                                                                                                                                                       WO200153312-A1
                                                                                                                                                                                                                                            chemokinetic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tcaaatctgaggccagagagtgtcgtcgctttgtccatccccagtggcagcttcttcac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
2000US-0488725.
2000US-0552317.
2000US-0598042.
2000US-0620312.
2000US-0653450.
2000US-0662191.
2000US-0693036.
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                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                               2000WO-US34263
                                                                                                                                                                                                                                           thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39.1%;
77.3%;
                                                                                                                                                                                                                                                                                                                            SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                               1132
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Pred. No. 2.:
                                                                                                                                                                                                                                                                                                                                                                                                               ВP
                                                                                                                                                                                                                                                                                                                              4990.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          355
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                                                                                                 AAD17476
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XPX
                                                                                                                  RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, activinyinhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 4990; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-NOV-2000; 2000US-0727344.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1132 BP; 274 A; 265 C; 285 G; 305 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C.N.S disorders.
              10-DEC-2001
                                                  AAD17476;
                                                                                    AAD17476 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            253
                                                                                                                                                                    327 catttatcagacaggt 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                           87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001-442253/47.
                                                                                                                                                                                                                                                                                                                                                                                                      atccacagcacaagtgaggcagacacagaaccctgtgtggatggctgggtatatgatcaa 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ggaatcetcagtgaagatgecetettgagaatetetateecaaetagaeteaaatetgagg 252
                                                                                                                                                                                                                                                                                                              atctccttctcatccaccatcgtgactgagtgggatctggtatgtgactctcaatcactg
                                                                                                                                                                                                                                                                                                                                                                                   ttccccaacacaagtgacgcagacatggagccctgtgtggatggctgggtgtatgacaga 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ccagagaagtgtcgttcgtttgtccatccccagtggcagcttcttcacctgaatgggact 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ggggccctcagccaagatgcactcttgagaatctccatcccactggactcaaacatgagg 86
                                                                                                                                                                                         catgtctcagacaggt 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ccagagaagtgtcgtcgctttgttcatcctcagtggcagctccttcacctgaatgggacc 146
                                                                                                                                                                                                                                         acttcagtggctamatttgtattcatggctggamtgmtggtgggaggcmtcctmggcggt 326
                                                                                                                                                                                                                                                            aaatcagtggttcaattcctacttctgactggaatgctggtgggaggcatcataggtggc 492
                                                                                                                                                                                                                                                                                                                                   agctacttcccttcgaccattgtgactaagtgggacctggtatgtgattatcagtcactg 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM41845
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wehrman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Asundi V, Chen R, Ma Y, Wehrman T, Xu C, Xue AJ, Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 232.8; DB 2
Pred. No. 2.7e-64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22; Length 1132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qian XB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ren F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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2 atggcattttctgaactcctggacctcgtgggtggcctgggcaggttccaggttctccag 61

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                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human transporter and ion channel-9 (TRICH-9) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-MAR-2000;
17-MAR-2000;
24-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; transporter and ion channel; TRICH-9; therapy; akinesia; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gastritis; inflammation; ss.
                                                                                                                                                                channels (TRICH-9) protein. The TRICH DNA, protein and their agonist and antagonists are useful in the diagnosis, treatment and prevention of transport disorders (akinesia, amyotrophic lateral sclerosis, cystic fibrosis), neurological (Alabeimer's disease, dementia, depression, epilepsy), muscle (e.g. cardiomyopathy, Becker's muscular dystrophy) or immunological disorders (e.g. allergies, acquired immunodeficiency syndrome (AIDS), Crohn's disease, rheumatoid arthritis, scleroderma, multiple sclerosis), viral, bacterial, parasitic, protozoal and helminthic disorders, cancer, anaemia, asthma, trauma, haemodialysis, helminthic disorders, cancer, anaemia, asthma, trauma, haemodialysis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-FEB-2001; 2001WO-US05942
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200162923-A2.
                                                                                                                                                                                                                                                                                                                                                                                     Thirteen human transporters and ion channels (referred to as TRICH-1 to TRICH-13), useful in the diagnosis, treatment and prevention of transport (e.g. akinesia), neurological, muscle or immunological disorders (e.g. allergies) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-FEB-2000;
02-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thornton M, Greene BD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yue H,
                                                                                                                                                                                                                                                                                                                                                      Claim 11; Page 127-128; 131pp; English.
                                                                                                                                                                                                                                                                                                                      The present sequence is a cDNA encoding human transporters and ion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; AAE10332.
                                                                                                                  Sequence 2455 BP; 416 A; 842 C; 707 G; 490 T; 0 other;
                                                                                                                                                     gastritis and inflammation.
                                                    Local Similarity
1 atggcctttgaggagctcttgagtcaagttggaggccttgggagatttcagatgcttcat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001-582050/65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Walia NK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; 2000US-0184866.
; 2000US-0187947.
; 2000US-0188333.
; 2000US-0190230.
; 2000US-0192077.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0193500.
                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= "Human TRICH-9 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lal P,
                                                        26.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gandhi AR, Tribo
BD, Hernandez R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Policky JL, Nguyen DB, Au-You
hi AR, Tribouley CM, Patterson
                                          0,
                                                          Score 208.8; DB 2
Pred. No. 2.3e-56;
                                            Mismatches 187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Borowsky ML,
                                                                           DB 22; Length 2455;
                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Au-Young J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sanjanwala MS;
                                                 0;
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                                                 Gaps
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RESULT 12
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                                                                                                     06-JAN-2000;
06-JAN-2000;
11-JAN-2000;
03-FEB-2000;
WPI; 2001-418355/44
                           Kato S,
                                                   (SAGA )
                                                                                            03-MAR-2000;
                                                                (PROT-) PROTEGENE INC
                                                                                                                                                                    28-DEC-2000; 2000WO-JP09359.
                                                                                                                                                                                                                           WO200149728-A2.
                                                                                                                                                                                                                                                                                                                                                          cell proliferation; immunomodulatory; autoimmune disorder; antimicrobial; multiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes; haematopoiesis; tissue growth activity; Parkinson's disease; cytostatic; Huntington's disease; Alzheimer's disease; chemotactic; chemokinetic; haemostatic; thrombolytic; tumour growth inhibitor; anabolic;
                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                             Human; hydrophobic domain; gene therapy; nutritional supplement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human protein having hydrophobic domain encoding cDNA clone HP03613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAD12566 standard; cDNA; 2865 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAD12566;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    482 gctgcgtgcggccctgcctcagacaggt 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  481 atcataggtggccatgtctcagacaggt 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                421 tatcagtcactgaaatcagtggttcaattcctacttctgactggaatgctggtgggaggc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 teggeegeegtgeeageeagetgetgggeaceeeteetggaeaacageaeggeteag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 gctgcagccattcctggtcatcgttgctgggtccacatgctggacaataatactggatct 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gtctatgaccgcagcatcttcacctccacaatcgtggccaagtggaacctcgtgtgtgac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gtatatgatcaaagctacttcccttcgaccattgtgactaagtgggacctggtatgtgat 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cccaatgccacggccaccagctggagcgaggccgacacggagccgtgtgtgggatggctgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ctgaatgggactatccacagcacaagtgaggcagacacagaaccctgtgtgggatggctgg 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tcaaatctgaggccagagaagtgtcgtcgttgttgtccatccccagtggcagcttcttcac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gccagcatcctagggagcttgagtcctgaggccctcctggctatttccatcccgccgggc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ggtaatgaaactggaatcctcagtgaagatgccctcttgagaatctctatcccactagac
                                                  SAGAMI CHEM
                         Kimura T;
                                                                                                     2000JP-0000585.
2000JP-0000588.
2000JP-0002299.
2000JP-0026862.
                                                                                         2000JP-0058367
                                                                                                                                                                                                                                                                                                                                                 antiinfertility; antiinflammatory; ss.
                                                                                                                                                                                                                                       /product= "Human protein having hydrophobic domain"
/note= "CDS is specifically is claimed in claim 3"
                                                                                                                                                                                                                                                                                        Location/Qualifiers 338..2074
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                                                   RES CENT
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Query Match Best Local

Local

Similarity

26.0%;

DB 22;

Length 2865;

Sequence 2865 BP; 488 A; 973 C; 830 G; 574 T; 0 other;

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The present sequence is human protein with hydrophobic domain encoding CC cDNA clone Hp03613. The polynucleotide and polypeptide of the invention CC associated with inappropriate polypeptide expression. The polynucleotides CC into a host cell and culturing the cell to expression. The polynucleotides CC into a host cell and culturing the cell to express the protein. The CC polynucleotides and its complementary sequences may also be used as DNA CC probes in diagnostic assays and also used in gene therapy. The CC properties may also be used as antigens in the production of antibodies are civity. The polypeptides and nucleic acids may be used as nutritional CC and in assays to identify modulators of polypeptide expression and CC supplements, to modulate cytokine and cell proliferation activity, to modulate immune stimulation or suppression (e.g. for the treatment of rheumatoid arthritis and insulin-dependent diabetes), to modulate complements of modulate cissue growth activity (e.g. for the creatment of parkinson's disease, Huntington's disease and Alzheimer's classes), to modulate activin and inhibin activity (e.g. for the creatment of parkinson's disease, Huntington's disease and Alzheimer's classes), to modulate chemotactic and chemokinetic activity, to modulate receptor induced activity, to modulate receptor to the controlling modulate haemostatic and thrombolytic activity, to modulate receptor to the controlling to the controlling modulate activity and inhibin activity to modulate receptor to the controlling modulate haemostatic and thrombolytic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; Page 252-257; 563pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alzheimer's and inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human proteins with hydrophobic domains and the nucleic acids encoding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         useful for preventing diagnosing and treating e.g. cancer
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818 gctgcgtgcggccctgcctcagacaggt 845
                  481 atcataggtggccatgtctcagacaggt 508
                                                                                                                     698 gtctatgaccgcagcatcttcacctccacaatcgtggccaagtggaacctcgtgtgtgac
                                                                                                                                                                                                    638
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                                                                                                                                                                                                                                                                                                                                                                            458 tcggccgccgtgcccagccaccgctgctgggcacccctcctggacaacagcacggctcag 517
                                                                                                                                                                                                                                                                                                                                                                                                 121 gctgcagccattcctggtcatcgttgctgggtccacatgctggacaataatactggatct 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 ctggtttttattcttccctcttctcatgttattaatccctcatatactgctagagaacttt 120
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                                                                            tatcagtcactgaaatcagtggttcaattcctacttctgactggaatgctggtggggggc 480
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Pred. No. 2.5e-56;
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neurological disorder; immune disorder; allergy; nootropic; dementia; AIDS; Acquired Immune Deficiency Syndrome; amyotrophic lateral sclerosis; cystic fibrosis; Alzheimer's disease; depression, epilepsy; scleroderma; cardiomyopathy; muscular dystrophy; Crohn's disease; multiple sclerosis; rheumatoid arthritis; cancer; anaemia; asthma; trauma; haemodialysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-FEB-2000;
02-MAR-2000;
09-MAR-2000;
17-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human transporter and ion channel-13 (TRICH-13) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAD17480 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gastritis; inflammation; cardiant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; transporter and ion channel; TRICH-13; therapy; akinesia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-DEC-2001
                                                                                                                    The present sequence is a cDNA encoding human transporters and ion channels (TRICH-13) protein. The TRICH DNA, protein and their agonist and antagonists are useful in the diagnosis, treatment and prevention of transport disorders (akinesia, amyotrophic lateral sclerosis, cystic fibrosis), neurological (Alzheimer's disease, dementia, depression, epilepsy), muscle (e.g. cardiomyopathy, Becker's muscular dystrophy) or immunological disorders (e.g. allergies, acquired immunodeficiency syndrome (AIDS), Crohn's disease, rheumatoid arthritis, scleroderma, multiple sclerosis), viral, bacterial, parasitic, protozoal and helminthic disorders, cancer, anaemia, asthma, trauma, haemodialysis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-FEB-2001; 2001WO-US05942
                                                                                                                                                                                                                                                                                                                               Thirteen human transporters and ion channels (referred to as TRICH-1 to TRICH-13), useful in the diagnosis, treatment and prevention of transport (e.g. akinesia), neurological, muscle or immunological disorders (e.g. allergies) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAR-2000;
                                                                                                                                                                                                                                                                                                   Claim 11; Page 130-131; 131pp; English.
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                                                                            Sequence 2047 BP; 363 A; 655 C; 598 G; 431 T; 0 other;
                                                                                                            gastritis and inflammation.
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 Local Similarity
nes 312; Conserv
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, Walia NK,
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2000US-0187947:
2000US-0188333.
2000US-0190230:
2000US-0190230.
2000US-0192077.
2000US-0193500.
Conservative
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hi AR, Tribouley CM, Patterson
   0;
 Score 180.8; DB 22;
Pred. No. 2.2e-47;
0; Mismatches 187;
      Indels
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 06-JAN-2000;
06-JAN-2000;
11-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                            Human; hydrophobic domain; gene therapy; nutritional supplement; cell proliferation; immunomodulatory; autoimmune disorder; antimicrobial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAD12607 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 gctgcagccattcctggtcatcgttgctgggtccacatgcttggaccaataatactggatct 180
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                                                                                                                                                                                                                                                                                                                                                      cell proliferation; immunomodulatory; autoimmune disorder; antimicrous multiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes; haematopoiesis; tissue growth activity; Parkinson's disease; cytostath haematopoiesis; tissue growth activity; Parkinson's disease; cytostath
                                                                                                                                                                                                                                                                                                                                                                                                                                     Human protein having hydrophobic domain encoding cDNA clone HP03882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                      Huntington's disease; Alzheimer's disease; chemotactic; chemokinetic; haemostatic; thrombolytic; tumour growth inhibitor; anabolic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 tcaaatctgaggccagagaagtgtcgtcgctttgtccatccccagtggcagcttcttcac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181
                                                                                                                                                                                                                                                                                                      contraceptive; antiinfertility; antiinflammatory; ss
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                                                                     28-DEC-2000;
                                                                                                       12-JUL-2001.
                                                                                                                                     WO200149728-A2
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   ; 2000JP-0000585.
; 2000JP-0000588.
; 2000JP-0002299.
                                                                     2000WO-JP09359
                                                                                                                                                                                                                      Location/Qualifiers 58..1710
                                                                                                                                                                      /*tag= a
/product= "Human protein having hydrophobic domain"
/product= "CDS is specifically is claimed in claim 3"
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                                                                                                                                                                                                                                                                                                                                                                 cytostatic;
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supplements, to modulate cytokine and cell proliferation activity, to modulate immune stimulation or suppression (e.g. for the treatment of microbial infections and autoimmune disorders such as multiple sclerosis, rheumatoid arthritis and insulin-dependent diabetes), to modulate tissue growth activity (e.g. for the treatment of Parkinson's disease, Huntington's disease and Alzheimer's disease), to modulate activin and inhibin activity (e.g. for controlling modulate haemostatic and thrombolytic activity, to modulate receptor.
                     361 gtatatgatcaaagctacttcccttcgaccattgtgactaagtgggacctggtatgtgat 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2194 BP; 408 A; 710 C; 615 G; 461 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polynucleotides and its complementary sequences may also be used as DNA probes in diagnostic assays and also used in gene therapy. The polypeptides may also be used as antigens in the production of antibodies and in assays to identify modulators of polypeptide expression and activity. The polypeptides and nucleic acids may be used as nutritional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is human protein with hydrophobic domain encoding CDNA clone HP03882. The polynucleotide and polypeptide of the invention may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. The polynucleotides into a host cell and culturing the cell to express the protein. The
                                                                                                                                                                                                       241 tcaaatctgaggccagagaagtgtcgtcgctttgtccatccccagtggcagcttcttcac 300
                                                                                                                                                                                                                                                   233 ----cggtttccacaaacatgacccccaaggcccttctgaccatctccatcccgccaggc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human proteins with hydrophobic domains and the nucleic acids encoding them, useful for preventing diagnosing and treating e.g. cancer, Alzheimer's and inflammation -
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03-MAR-2000; 2000JP-0058367.
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gtctatgaccgcagcgtcttcacctccaccatcgtggccaagtgggacctggtgtgcagc
                                                                                                         ctgaatgggactatccacagcacaagtgaggcagacacagaaccctgtgtgggatggctgg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  activity, to modulate inflammation and to inhibit tumour growth.
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Pred. No. 2.2e-47;
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                                                                                                                                                                                                                                                                                                        The present sequence encodes a human placental organic anion transporter designated OAT4. OAT4 has nephrotrophic activity. The OAT4 protein and encoded gene are useful in studying causes of abnormality, including the application of a variant nucleic acid as a probe to detect the presence of a gene encoding the transporter OAT4, or to identify or quantify such gene, and in developing drugs to prevent or treat various kidney diseases and abnormal foetal growth.
                                                                                                                                                                                                                                                                             Sequence 2210 BP; 426 A; 709 C; 614 G; 461 T; 0 other;
           173
                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 5; Page 23-26; 32pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Placental organic anion transporter gene and encoded polypeptide OAT4, useful in studying causes of abnormality, and in developing drugs to prevent or treat various kidney diseases and abnormal fetal growth -
               121 gctgcagccattcctggtcatcgttgctgggtccacatgctggacaataatactggatct 180
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в1332219 602981678	BI332	1	807	33.	265.8	19	
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## ALIGNMENTS

MEDLINE COMMENT VERSION KEYWORDS LOCUS
DEFINITION
ACCESSION RESULT AV652088 REFERENCE FEATURES SOURCE ORGANISM TITLE AUTHORS JOURNAL source Contact: Zeguang Han Chinese National Human Genome Center at Shanghai 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China Tel: 86-21-50801919(ex.45) Fax: 86-21-50801922. AV652088 GLC Homo sapiens AV652088 GLC Homo sapiens AV652088 Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W., Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Gu,J., Chen,Z. and Han,Z.

Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Homo sapiens AV652088.1 GI:9873102 EST. 1 (bases 1 to 615) numan. l: hanzg@chgc.sh.cn clone is available at CHGC Location/Qualifiers /note="Vector: pBluescript sk(-); Site\_1:
xhor" /organism="Homo sapiens" /db\_xref="taxon:9606" /clone="GLCCWF10" /tissue\_type="corresponding non cancerous liver tissue"
/dev\_stage="Adult" /lab\_host="SOLR" /clone\_lib="GLC" 615 bp mRNA linear EST 15-JAN-2 cDNA clone GLCCWF10 3', mRNA sequence. in Shanghai. EcoRI; Site\_2: EST 15-JAN-2002

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KEYWORDS
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(E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC en was generated during the R&D process and may have higher chance of
                                                            Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); and Chemical Research (RIKEN), Tokohama, Kanagawa 230-0045, Japan 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-045, Japan
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                                                                                                                                  Fujiyama,A., Hattori,M., Toyoda,A.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
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troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male Library clone:PTB-106L08.F. troglodytes
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Pred. No. 1.1e-116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 392;
 J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., Watte,Y., Wylie,T., Waterston,R. and Wilson,R. Theising,B., Washu-NCI human EST Project
Unpublished (1997)
Contact: wilcon.
                                                                             Mammalia; Eutheria; Primates; Cai
1 (bases 1 to 39)
Hillier,L., Allen,M., Bowles,L.,
Krizman,D., Kucaba,T., Lacy,M.,,
                                                                                                                                                                                                                                                AA680184 399 bp mRNA linear EST 19-DEC-
zillc10.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA
clone IMAGE:430482 3' similar to TR:G1293672 G1293672
KIDNEY-SPECIFIC TRANSPORT PROTEIN. ;, mRNA sequence.
                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                    AA680184.1 GI:2656651
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/clone_lib="PTB Chimpanzee Male BAC Library"
160 c 154 g 207 t 5 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="PTB-106L08.F"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Pan troglodytes"
/db_xref="taxon:9598"
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Pig.
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Email: clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMAGE Consortium (info@image.llnl.gov) fo
Seq primer: -40ml3 fwd. ET from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                           MARC 1PIG Sus scrofa
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100 c 72 g 132 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
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/lab_host="DH10B (ampicillin resistant)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE:430482"
                                         GI:15031939
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99.7%;
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                  421 tatcagtcactgaaatcagtggttcaattcctacttctgactggaatgctggtgggaggc
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                                                                                                                                                                                                                                                                                                                                                                                  gctgcagccattcctggtcatcgttgctgggtccacatgctggaccaataatactggatct 180
TATCAGTCTCAGAAACCACTGGTCCAATTTGCATTCATGGCTGGAATGCTGCTGGGAGGC
                                                                                       gtatatgatcaaagctacttcccttcgaccattgtgactaagtgggacctggtatgtgat
                                                                                                                                          CTGAATGGAACCTTCCCCAATGTGACTGATCTGGACACGGAGCCCTGTGTGGACGGCTGG
                                                                                                                                                                  ctgaatgggactatccacagcacaagtgaggcagacacagaaccctgtgtggatggctgg
                                                                                                                                                                                                               TCAAACTTGAAGCCAGAGAAATGTCGGCGCTACCTCCACCCCCAGTGGCAGCTCCTTCAC
                                                                                                                                                                                                                                                                                                                      ggtaatgaaactggaatcctcagtgaagatgccctcttgagaatctctatcccactagac
                                                                                                                                                                                                                                                                                      GGTAATGACATGGGGACCCTCGGCCCCGAGGTTCTCCTGAGAATCTCCATCCCCTGGAC
                                                                                                                                                                                                                                                                                                                                                           ACAGCGGCCATTCCTGGTCATCACTGCTGGGTCCGCATCCTCGACAATGACACTGACTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                ATGCTTTTAGCCTTTCCCCCCCCCATGATGGTAGTCTGTCATATTCTGTTGGAGAATTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGGCTTTTGAGGAGCTCCTGAATGAAGTCGGTGGCTTGGGGAAATTCCAGATGCTTCAG 128
                                                                     GTGTATGACCAAAGCTCCTTCTCCCACACCATCGTGACTGAGTGGGACCTCGTATGTGAT
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PO Box 166, Clay Center, N
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stone, R.T., Heaton, M.P., and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Design and use of two pooled tissue normalized cDNA libraries for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria; Cetartiodactyla; Suina; 1 (bases 1 to 581) Frahrenkrug, S.C., Freking, B.A., Rohrer, G.A.,
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Seq primer: ATTTAGGTGACACTATAG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 1PIG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="pooled"
/lab_host="DH10B"
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Pred. No. 1.2e-
D; Mismatches
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AA682573/c
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
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             TCATAGTTGCCCATGTCTCAGACAGTTGGCTGGTGGAATCTGCTCGGTGGTTGATAATCA 304
                                                                                                              320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@mage.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Seq primer: -40ml3 fwd. ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. I Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA682573 367 bp mRNA linear EST 19-
zj20a06.s1 Soares_fetal_liver_spleen_lNFLS_S1 Homo sapiens
clone IMAGE:450802 3' similar to TR:G1293672 G1293672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 303.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   White, Y., Wylie, T., Watersto
WashU-NCI human EST Project
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 367)
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                                                                                                                                                                                                                     constructed by Bento Soares and M.Fatima Bonaldo." 88 c 66 g 127 t
                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:450802"
                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="20 week-post conception fetus"
                                                                                                                                                                                                                                                                                                                                                                                                /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Soares_fetal_liver_spleen_1NFLS_S1"
                                                                                                                          38.2%;
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Pred. No. 1.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://lmage.llni.gov
plate: LLAM10958 row: o column: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence start: 13
High quality sequence stop: 819.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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BG972774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
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Conservative
                                                                                                                                                    /Clone="IMAGE:4972265"
/Clone=lib="NCI_CGAP_Kid14"
/Clone_lib="NCI_CGAP_Kid14"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: kidney; Vector: pCWV-SPORT6; Site_1: NotI;
/site_2: SalI; Cloned unidirectionally. Primer: Oligo dT
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. | "
a 197 c 185 g 247 t
                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/strain="FVB/N"
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                           36.5%;
73.6%;
0;
                     Score 293.6;
Pred. No. 4.8
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 1054)
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BF783752
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National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                          found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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                                                                                       /Clone_lib="NCI_CGAP_Kid14"
//lab_host="DH10B (TI phage=resistant)"
/lab_host="DH10B (TI phage=resistant)"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally, Primer: Oligo dT
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Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
                                                                                                                                                                                  Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Sushiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jap Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2001)
Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                   Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Muramatsu, M. and Hayashizaki, Y., RIKEN Mouse ESTS (Arakawa, T., et al. 2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
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                                                                                                                                                       81-45-503-9216
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241 tcaaatctgaggccagagaagtgtcgtcgctttgtccatccccagtggcagcttcttcac 300
                                                                                                                                                                    205 ACTGCAGCCATTCCTAGTCATCGCTGCTGGGTCCCCATCCTTGACAATGACACTGCCTCT 264
                                                                                                                                                                                                     121 gctgcagccattcctggtcatcgttgctgggtccacatgctggacaataatactggatct 180
                                                                                                                                                                                                                                                                                   145 ATGATATTTGTGTTAATCTGCCATGCCCTGTCGGCTCCTCACACTCTTTTGGAGAACTTC 204
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                                                                                                                                                                                                                                                                                                                                         61 ctggtttttattcttccctctcatgttattaatccctcatatactgctagagaacttt 120
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                                                     GATAATGGCAGTAGGATCCTGAGCCAAGATGACCTCCTGAGGATCTCCATCCCCCTGGAC 324
                                                                                         99taatgaaactggaatcctcagtgaagatgccctcttgagaatctctatcccactagac 240
                                                                                                                                                                                                                                                                                                                                                                                                     ATGGCCTTTCAGGACCTTATAATTCAAATTGGCAGCTTGGGGAGGTTCCAGATTCTTCAC 144
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RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. . 10 (10), 1617-1630 (2000) wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hayashizaki,Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Computational Analysis of Full-Length Mouse cDNAs Compared with Juman Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Note-"Site_1: Sal1; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="kidney"
/dev_stage="0 day neonate"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:10090"
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72.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
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      61 ctggtttttattcttccctctctcatgttattaatccctcatatactgctagagaacttt 120
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                                                                          1 atggcctttgaggagctcttgagtcaagttggaggccttgggagatttcagatgcttcat 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     481 atcataggtggccatgtctcagacaggtggctggtggaatct 522
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                                                                                                                                                                      Local
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                                                  ATGGCCTTTCAGGAACTCCTGAATCAAGTTGGAAGCCTAGGAAGATTCCAGATCCTTCAG 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCTCAGGCACTGAATTCAGTGGCTAAATNTATATACATGACTGGTATCTNTATAGGATAT 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGAATGGCACCTTCCCCACTGTAACAGAGCCAGACACAGAGCCCTGTGTGGATGGCTGG 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCCAACCTGAGACCGGATAAATGCCGTCGCTATATTCAACCACAGTGGCATCTCCTTCAT 384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://image.llnl.gov
Plate: LLAM11122 row
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5', mRNA sequence.
BI102429
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        quality sequence stop:
                                                                                                                                                                                                                                                         /clone="IMAGE:5044850"
/clone_lib="NCI_CGAP_Kid14"
/clone_lib="NCI_CGAP_Kid14"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally Primer: Oligo dT
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. | "
a 206 c 189 g 268 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                               36.0%;
72.9%;
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****** of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                         0;
                                                                                                                                                           Score 289.2; DB 1
Pred. No. 6.5e-64;
                                                                                                                                         Mismatches
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                                                                                                                                         138;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 ggtaatgaaactggaatcctcagtgaagatgccctcttgagaatctctatcccactagac 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  293 ACTGCAGCCATTCCCAATCATCGCTGCTGGGCCCCCATCCTTGACAATGACACTGCCTCT 352
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                                                                                                                                                                                                                                             source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 739)
Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person
,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter
,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
Waterston,R. and Wilson,R.
The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEMBRANE TRANSPORT PROTEIN. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                             Fax: 314 A00 TOTAL PROPERTY FA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
Other_ESTs: um18h07.x1
                                                                                                                                                                                                                                                                                                              High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nouse mouse.
                                                                                                                                                                                                                                                                                                                                                   primer: custom primer used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           314 286 1800
314 286 1810
/clone_lib="Sugano mouse kidney mkia"
/sex="female"
/dev_stage="adult"
                                                                                                                                                                           /organism="Mus musculus"
/strain="C57BL"
                                                                                                         /db_xref="taxon:10090"
/clone="IMAGE:2192701"
                                                                                                                                                                                                                                                                          Location/Qualifiers
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                  241 tcaaatotgaggccagagaagtgtcgtcgctttgtccatccccagtggcagcttcttcac 300
                                                                                                                                                                                                                                                                 527 TTGAATGGCACTTTCTCCAATGTGTCAGAGCCAGACACTGAGCCCTGTGTGGATGGTTGG 586
                                                                                                                                                                                                                                                                                                301 ctgaatgggactatccacagcacaagtgaggcagacacagaaccctgtgtggatggctgg 360
                                     481 atcataggtggccatgtctcagacaggt 508
                                                                                                                            421 tatcagtcactgaaatcagtggttcaattcctacttctgactggaatgctggtgggaggc 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 ctggtttttattcttccctctctcatgttattaatccctcatatactgctagagaacttt 120
707 ATCATATGTGGCCATCTGTCAGACAGGT 734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 atggcctttgaggagctcttgagtcaagttggaggccttgggagatttcagatgcttcat 60
                                                                                                                                                                                                                                                                                                                                                                                                                                               GATAATGGCAGTAGGATACTGAGCCAAGATGACCTCCTGAGGATCTCCATCCCCCTGGAT 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ggtaatgaaactggaatcctcagtgaagatgccctcttgagaatctctatcccactagac 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACTICCAGCCATTCCCAATCATCGCTGCTGGGTCCCCATCCTTGACAATGACACTGCCTCT 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gctgcagccattcctggtcatcgttgctgggtccacatgctggaccaataatactggatct 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATAGTTTTTCTTTTCCTCCTCAATGCCATTGTAGTACCACATATTGGAATGGAGAACTTT 346
                                                                                      TCTCANGCACTGAATTCTGTCACTAAATAATCATTCATGATTGGCCTATNNTATAGNGGT 706
                                                                                                                                                                                                    gtatatgatcaaagctacttcccttcgaccattgtgactaagtgggacctggtatgtgat 420
                                                                                                                                                                                                                                                                                                                                                        TCCAACCTGAGACTGGATAAATGTCGTCGTTTTGCCCAACCACAGTGGCATCTTCTTCAT 526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAGCACA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 be used to isolate the cDNA insert. Size selection performed to exclude fragments <1.5kb. Library
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72.2%;
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Pred. No. 8.7e-63;
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BC016496 1914 bp mRNA linear HTC 05-NOV-200 Mus musculus, Similar to solute carrier family 22 (organic cation transporter)-like 2, clone IMAGE:4236791, mRNA.

HTC 05-NOV-2001

BC016496.1 GI:16741330

house mouse.

Strausberg, R.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1914)

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421 tatcagtcactgaaatcagtggttcaattcctacttctgactggaatgctggtgggaggc 480
                                                                                                                                      455 TTGAATGGCACTTTCTCCAATGAGACAGAGCCAGACACTGAGCCCTGTGTGGATGGTTGG 514
                                                                                                                                                                   301 ctgaatgggactatccacagcacaagtgaggcagacacagaaccctgtgtgggatggctgg 360
                                                                                                                                                                                                                                                             241 tcaaatotgaggccagagaagtgtcgttgtcgctttgtccatccccagtggcagcttcttcac 300
                                                                                                                                                                                                                                                                                                                              336 GATAATGCCAGTAGGATCCTGAGCCAAGATGACCTCCTGAGGATCTCCATCCCCCTGGAT 395
                                                                                                                                                                                                                                                                                                                                                                                                                       276 ACTGCAGCCATTCCCAATCATCGCTGCTGGGCCCCCATCCTTGACAATGACACTGCCTCT 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 gctgcagccattcctggtcatcgttgctgggtccacatgctggacaataatactggatct 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 ctggttttttattcttccctctctcatgttattaatccctcatatactgctagagaacttt 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                   gtatatgatcaaagctacttcccttcgaccattgtgactaagtgggacctggtatgtgat 420
                                             GTGTATGACAGGAGCAACTTCCTTTCTACCATTGTGACTGAGTGGGGACCTGGTGTGTGAA 574
                                                                                                                                                                                                                                  TCCAACCTGAGACTGGATAAATGTCGTCG-TTTGCCCAACCACAGTGGCATCTTCTTCAT 454
                                                                                                                                                                                                                                                                                                                                                        99taatgaaactggaatcetcagtgaagatgccetcttgagaatetetateccactagac 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 31 Row: e Column: 7
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein This clone has the following problem: frame shifted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: villalon@bcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,
A.M., Holloway, M., Telford, B, Hodgson, A., Bouck, J., Yu, W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Muzny, D.M., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www.hgsc.bcm.tmc.edu/cdna/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tissue Procurement: Jeffrey E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (31-OCT-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center code: BCM-HGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pcmv-sport6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="IMAGE:4236791"
/tissue_type="Kidney, normal.
/clone_lib="NCI_CGAP_Kid14"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/db_xref="taxon:10090"
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73.6%;
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) KONDO, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
wastahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Muramatsu, M. and Hayshizaki, Y.

RIKIN Mouse ESTs (Arakawa, T., et al. 2001)

Uppublished (2001)

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                       further details.
                                                                                                                                                                                                                                                                                                                                                              Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hayashizaki,Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                   e mouse tissues.
                                                                                                                                                                                                                                                                                                                                                                                                  Computational Analysis of Full-Length Mouse cDNAs Compared with uman Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arakawa T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagama, A., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T.,
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/tissue_type="kidney"
/dev_stage="0 day neonate"
                                                                           kidney"
                                                                                         /clone_lib="RIKEN full-length enriched,
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                                                                                                                                                                                                    'organism="Mus musculus"
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          238 ACTGCAGCCATTCCTAGTCATCGCTGCTGGGTCCCCATCCTTGACAATGACACTGCCTCT 297
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A15300
                                                                                                                   EST
                                                                                                                                                                                                                       TRANSPORTER 1. ;, mRNA sequence.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                   AI530049.1 GI:4444184
                                                                           house mouse.
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                                                                                                                                                                                                                                                                                                                                                                                                  238 CTCTTTTGTTCTCTTCCTCGTAGGCCTTGTGGTACCTCATATTACAATGGAGAACTTTAC 297
                                                                                                                                                                                                                     183 taatgaaactggaatcctcagtgaagatgccctcttgagaatctctatatcccactagactc 242
                                                                                                                                                                                                                                                                                                                           123 tgcagccattcctggtcatcgttgctgggtccacatgctggacaataatactggatctgg 182
                                                                               418 CAACCTGAGACTGGATAAATGTCGTCGTTTTGCCCAACCACAGTGGCATCTTCATTT
                                                                                                                                                                                     358 TAATGGCAGTAGGATCCTGAGCCAAGATGACCTCCTGAGGATCTCCATCCCCTGGATTC 417
303 gaatgggactatccacagcacaagtgaggcagacacagaaccctgtgtggatggctgggt 362
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1 (bases 1 to 974)

Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., E., Staller,T., Gibbons,M., Pape,D., Allen,M., Bowers,Y., Person B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,B., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R., and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Porest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The WashU-NCI Mouse EST Project 1999
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This clone is available royalty free through LLNL; contact the
                                                                                                                                                                                                                                                                                            TGCAGCCATTCCCAATCATCGCTGCTGGGCCCCCATCCTTGACAATGACACTGCCTCTGA 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq primer: custom primer used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 was primed with an oligo(dT) primer was primed with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was [ATGTGGCCTTTTTTTTTTTTTTTTT]; double-stranded, digested ligated to a Draill adaptor [TGTTGGCCTACTGG], digested ligated to a Draill sites of the pME18S-FL3 and cloned into distinct Draill sites of the pME18S-FL3 and cloned into distinct Draill sites (ACCATGTG), Xhol show vector [5] site CACTGTGTG, 3 site CACCATGTG), Xhol show vector [5] site CACTGTGTG, 3 insert Size selection was be used to isolate the cDNA insert Size selection was
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                                                                          Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Salto, T., Kiyosawa, H., Yamanaka, I., Aizaw Hayashizaki, Y., Hara, A., Itoh, M., Kawal, J., Shibata, K. and
                                                                                                                                                                                                                                                                                                                         Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
Watchiki,M., Yoneda,Y., Isnue,K., Togawa,Y., Izawa,M., Ohara,E.,
S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
                      Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
                                                                                                                                                                                                                           RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Feat: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shihata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Muramatsu, M. and Hayashizaki, Y. RIKEN Mouse ESTS (Arakawa, T., e Unpublished (2001)
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    visit our web site (http://genome.gsc.riken.go.jp) for
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203 ATGGCCTTTCAGGAACTCCTGAATCAAGTTGGAAGCCTAGGAAGATTCCAGATCCTTCAG 262
61 ctggtttttattcttccctctctcatgttattaatccctcatatactgctagagaacttt 120
                                               l atggcctttgaggagctcttgagtcaagttggaggccttgggagatttcagatgcttcat 60
                                                                                                                    Similarity
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                                                                                                                                                                                         176 a
                                                                                                   Conservative
                                                                                                                                                                        was cleaved with BanHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC Tissue was provided by William A. Held, Roswell Park Cancer Institute, Department of Molecular and Cellula Biology, Elm and Carlton Streets, Buffalo, NY 14263, assistance we gratefully acknowledge."

156 g 202 t l others
                                                                                                                                                                                                                                                                        /lab_host_"DH10B"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev_stage="adu]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="liver tumor"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="RIKEN full-length enriched, adult male liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="C730048C13"
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                                                                                                               34.6%;
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                                                                                                            Score 278.2; DB 9;
Pred. No. 4.3e-61;
                                                                                        Mismatches 134; Indels
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MEDLINE
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Best Local Similarity 74.6%;
Matches 367; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
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                                                                                       tcctcagtgaagatgccctcttgagaatctctatcccactagactcaaatctgaggccag 256
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                                                                                                                                                                                                                                                                                                   tcttgagtcaagttggaggccttgggagatttcagattgcttcatctggtttttattcttc 76
AGAAGTGTCATCGCTTCCTCCACCCCCAGTGGCAGCTCCTTCACCTGAATAGGACCTTCG 293
                                                                    TCCTCAGCCCTGATGTCCTCCTGAGAATCTCCATCCCACTGGATTCAAACTTAAAGCCAG
                                                                                                                                           GTCATCGCTGCTGGGTCTACATCCTGGA-----TAATGCCACTGAGA 173
                                                                                                                                                                                                                                                                                    TCCTTAATGAAGTTGGTGGCCTGGGAAAATTCCAGATCCTTCAGATGGTTTTAGCTCTTC 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fukushima
Tel: 81-248-25-5641
Fax: 81-248-25-5725
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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5', mRNA
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EST.
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AV605334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: kazusugi@cocoa.ocn.ne.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Yoshikazu Sugimoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic Acids Res. 29 (22), E108 (2001) 21570554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Establishment of a high throughput EST sequencing system using poly(A) tail-removed cDNA libraries and determination of 36,000
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and Sugimoto,Y.
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was deleted from a Not1 site"
164 c 137 g 160 t
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/tissue_type="kidney"
/dev_stage="fetus"
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/db_xref="taxon:9913"
/clone="ElKI028B10"
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Search completed: July 1, 2002, 14:44:48
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 atggcctttgaggagctctt.....acacaaaagtgaccaaattt 804
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2 US-08-647-397-1
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1 US-08-32-463-14
1 US-08-31-15
2 US-09-681-320-1
2 US-08-658-665-178
2 US-08-68-101-39
2 US-08-23-95-11-1
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2 US-08-314-979-1
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3 US-08-314-716-1
3 US-08-316-713-3
3 US-08-655-655-3
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2 US-08-91-789A-176
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                             Sequence 48, Appl
Sequence 1, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 15, Appl
Sequence 178, Appl
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Sequence 1, Appli
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; LOCATION:
US-08-647-397-1
                                                                                                                                   Sequence 14, Application US/08232463 Patent No. 5670367
                       GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 122;
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INFORMATION FOR SEQ ID NO: 1:
            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRAGMENT TYPE: internal ORIGINAL SOURCE: ORGANISM: Mus musculus
                                                                                                                                                                                                                                523 TTGGAGGACCTGTGTTTGGAGAACTGTCAGACAGGT 558
                                                                                                                                                                                                                                                  473 tgggaggcatcataggtggccatgtctcagacaggt 508
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HYPOTHETICAL: N
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LENGTH: 2102 base pairs
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TELEFAX: 617-720-2441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Gates, Edward R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: B0)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-D
SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/647,397
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Conservative
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SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
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Pred. No. 2.5e-07;
0; Mismatches 88; Indels 6
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TELEX: 899149
INFORMATION FOR SEQ ID NO:
                                           1124 RRRRRRRRRRRRRRRRRRRRRRRRR 1098
                                                                                                      1484 TGTAATTACCTATCTATGCAAGTAGTTAAAGAGATAGAAGAATTTGGTACRRRRRRRRR 1425
                                                                         775 aatgattgctacacaaaagtgaccaaa 801
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
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                                                                                                                                     715 cgtaaaaggatctgtatcctggtattttttgagaaaaaaatctcaaggaaaaggcataaa 774
                                                                                                                                                                                                       655 gagctggatgcagcacagaccaaaactactgtgtgtgacttgttccgcaaccccagtatg 714
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LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: EP 91 114 300.6 FILLING DATE: 26-AUG-1991 ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE:
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CITY: Alexandria
STATE: VA
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                                                                                                                                                                                                                                                                            ggaataaagaatgctgaagaaaccctgaacatagaggttgtaagatccaccatgcaggag 654
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APPLICANT: DORNER
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: (703)836-9300
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141 tcgttgctgggtccacatgctggacaataatactggatctggtaatgaaactggaatcct 200
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                           261 gtgtcgtcgctttgtccatccccagtggcagcttcttcacct 302
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                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
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US-07-906-871-15/c
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; Patent No. 5340739
; LOCATION:
US-07-906-871-15
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INFORMATION FOR SEQ ID NO:
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TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US89/03051
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07
FILING DATE: 03 JAN 1992
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: (202)833-7533
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                                                                                                                                             FEATURE
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REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0627.2830004
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18-JAN-1991
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                                                                                   Matches
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                                                                                                                                                                                                                                                                                           TELEFAX: (716) 263-1600 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Gonsalves, Dennis
APPLICANT: Meng, Baozhong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
7764 GGCTGAATGGCAAGTCAAATTGGGAAACTCCCCGGTGAATCAAATGAGGCTTTTGAAGCC 7823
                                                                                                                                                                                       TOPOLOGY: 15
MOLECULE TYPE:
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                      559 ggcttaaaggcacttagaaaagttgcacgcacaaatggaataaaggaatgctgaaggaaacc 618
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                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1304
                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 60
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: GOLdman, Michael L.
REGISTRATION NUMBER: 30,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14698 CAACATGTTAAATACTGAGCAGAGGAAAAAGCCACAACCAGAGAAGTAGGAAGAAACAGGA 14639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: RUPESTRIS STEM PITTING ASSOCIATED VIRUS
                                                                                            Local Similarity 50.0%;
                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          647 tgcaggaggagctggatgcagcacagaccaa 677
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                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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                                                                             83; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rochester
                                                                                                                                                                                                                                                    8743 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Nixon, Hargrave, Devans & Doyle LLP Clinton Square, P.O. Box 1051
                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nixon,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     US 60/069,902
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US/09/081,320
                                                                                                                                                                                                                                                                                                                                                                             30,727
                                                                    Score 33.2; DB 3; Length 8743; Pred. No. 1.7; 0; Mismatches 83; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                19603/1722
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0; Mismatches
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                                                                        0;
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                                                                        Gaps
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2083 AAAGCTGTAGATTTTTCCAGAATGGATATTAAGGGAGATGATATTAGCAAAATGGGAATA 2142
                                                                                                                                                 1964 AAGAAGATTTAGTAAACGAATTAATTGAAAATACCAATAGTTTCGAAGATATAATGACTA 2023
                                                                                                                                                                                                                          1904 AATTGGTAGACAGAAAATATTATCTAAACCAGATACGTCTAAAACAGAAATAGAGATTA 1963
                                                                        2024 TACCTACCAGTATCCCTATGAGATA-TTTTTTTAAACCGGTACTAAGAGAAAAAGTATCT 2082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Frommer Esq., William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 45431
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)840-3333
                                 728 gtatcctggtatttttgagaaaaaaatctcaaggaaaaggcataaaaatgattgctaca 787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Recombinant TITLE OF INVENTION: Compositions and Uses
                                                                                                          668 cacagaccaaaactactgtgtgtgacttgttccgcaaccccagtatgcgtaaaaggatct 727
                                                                                                                                                                         608 ctgaagaaaccctgaacatagaggttgtaagatccaccatgcaggaggaggagctggatgcag 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Paoletti, Enzo
APPLICANT: Pincus, Steven E.
APPLICANT: Cox, William I.
APPLICANT: Kauffman, Elizabeth K.
                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                679 actactgtgtgtgacttgttccgcaaccccagtatgcgtaaaagga 724
                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 5798 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  619 ctgaacatagaggttgtaagatccaccatgcaggaggagctggatgcagcacagaccaaa 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX:
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 05 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
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                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (212)840-0712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                       DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUN-1996
                                                                                                                                                                                                                                                                                                                            4.0%;
48.0%;
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                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                      Score 32.4; DB 2; Length 5798; Pred. No. 2.5;
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                                                                                                                                                                                                                                                                                                   Mismatches 131; Indels
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788 caaaagtgaccaaa 801

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US-08-796-101-39
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Patent No. 6183752
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                    Query Match 4.0%; Score 32.4; DB 4; Length 5798; Best Local Similarity 48.0%; Pred. No. 2.5; Matches 122; Conservative 0; Mismatches 131; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (212) 764-5574
INFORMATION FOR SEQ ID NO:
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APPLICANT:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/796,101
FILING DATE: 05-FEB-1997
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ADDRESSEE: CURTIS, MORRIS & SAFFORD, P.C.
STREET: 530 FIFTH AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: KOWALSKI, THOMAS J
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: ERDILE, LORNE
APPLICANT: PINCUS, STEVEN
TITLE OF INVENTION: RESTENOSIS/ATHEROSCLEROSIS DIAGNOSIS,
TITLE OF INVENTION: PROPHYLAXIS AND THERAPY
NUMBER OF SEQUENCES: 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 5798 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                    1904 AATTGGTAGACAGAAAATATTATCTAAACCAGATACGTCTAAAACAGAAATAGAGATTA 1963
                                                                                                                                                                    1964 AAGAAGATTTAGTAAACGAATTAATTGAAAATACCAATAGTTTCGAAGATATAATGACTA 2023
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2083 AAAGCTGTAGATTTTTCCAGAATGGATATTAAGGGAGATGATATTAGCAAAATGGGAATA 2142
                                                                                  2024 TACCTACCAGTATCCCTATGAGATA-TTTTTTTAAACCGGTACTAAGAGAAAAAGTATCT 2082
                                                                                                                                                                                                                                                                             608 ctgaagaaaccctgaacatagaggttgtaagatccaccatgcaggaggaggtggatgcag 667
                                     728 gtatcctggtatttttgagaaaaaaatctcaaggaaaaggcataaaaatgattgctaca 787
                                                                                                                     668 cacagaccaaaactactgtgtgtgacttgttccgcaaccccagtatgcgtaaaaggatct 727
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SPEIR, EDITH
ZHOU, YI FU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (212) 840-3333
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RESULT 9
US-07-923-095-1
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TELEPHONE: 203-321-2971
TELEX: 710-474-4059
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1730 base pairs
                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Sokol Dr., Kurania R.
APPLICANT: Ziai Dr., Mohammad R.
APPLICANT: Ziai Dr., Mohammad R.
THYEN OF INVENTION: Nucleic Acid Sequence Encoding an Apamin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2143 AAACACGGAGAAAA 2156
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ATTORNEY/AGENT INFORMATION:
NAME: Lowney Dr Kannon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION:
TELEPHONE: 203-321-2361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATE PATENTIA Release #1.0, Version #1.25
SOFTWARE: PATENTIAN PATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      788 caaaagtgaccaaa 801
                                                                                                                                               1529 CCCTTTATGGTGGGCTTTGTTTGTTTTAAAGCCACGGACAATGGCACAGCTTACCTCAG 1588
                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE:
                                                                     1589 TGGGAGATGCAAGATGAGTACCAGGGGGTGGTTAGGAATAATTTCTAAGTTTTTCCACCT 1648
1649 TGAATGCTGAGTGG 1662
                                                                                                                                                                    343 ccctgtgtggatgggtatatgatcaaagctacttcccttcgaccattgtgactaag 402
                 463 ggaatgctggtggg 476
                                                                                                       403 tgggacctggtatgtgattatcagtcactgaaatcagtggttcaattcctacttctgact 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 19920
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                                                                                                                                                                                                                      y Match 3.9%; Score 31.6; DB 1; Length 1730;
Local Similarity 52.2%; Pred. No. 2.4;
hes 70; Conservative 0; Mismatches 64; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                       LOCATION:
                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
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140..1456
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                   Sequence 1, Application US/08314979 Patent No. 5607843
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Best Local Similarity
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            Matches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08229511 Patent No. 5591824
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                                                                                                                              1649 TGAATGCTGAGTGG 1662
                                                                                                                                                                                                                                                                         1529 CCCTTTATGGTGGGCTTTGTTTGTTTTAAAGCCACGGACAATGGCACAGCTTACCTCAG 1588
                                                                                                                                                                                                1589 TGGGAGATGCAAGATGAGTACCAGGGGGTGGTTAGGAATAATTTCTAAGTTTTTCCACCT 1648
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FILING DATE: 30-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/923,095
FILING DATE: 30-JUL-1992
ATTORNEY/AGENT INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                      463 ggaatgctggtggg 476
                                                                                                                                                                                                                              403 tgggacctggtatgtgattatcagtcactgaaatcagtggttcaattcctacttctgact 462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 1730 base pairs
                                                                                                                                                                                                                                                                                                343 ccctgtgtgggatgggtatatgatcaaagctacttcccttcgaccattgtgactaag 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: cDNA
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ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: 2 Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Chandra, Manik
TITLE OF INVENTION: Apamin Binding Protein/Receptor
NUMBER OF SEQUENCES: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 140..1456
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Sokol, Patricia Tyson
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Sequence 1, Application US/08436716 Patent No. 5652111 GENERAL INFORMATION:

APPLICANT:

Sokol Dr., Patricia T.

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US-08-436-716-1
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US-08-314-979-1
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TITLE OF INVENTION: Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 203-321-2971
TELEX: 710-474-4059
INFORMATION FOR SEQ ID NO:
                                                             1649 TGAATGCTGAGTGG 1662
                                                                                                                                                                              1529 CCCTTTATGGTGGGCTTTGTTTGTTTTAAAGCCACGGACAATGGCACAGCTTACCTCAG 1588
                                                                                                                            1589
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                                                                                                                                        403 tgggacctggtatgtgattatcagtcactgaaatcagtggttcaattcctacttctgact 462
                                                                                                                                                                                                     343 ccctgtgtggatggctgggtatatgatcaaagctacttcccttcgaccattgtgactaag 402
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                                                                                      463 ggaatgctggtggg 476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1730 base pair
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Pig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Lowney Dr., Karen REGISTRATION NUMBER: 312 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 07/923,095
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                                                                                                                  TGGGAGATGCAAGATGAGTACCAGGGGGTGGTTAGGAATAATTTCTAAGTTTTTCCACCT 1648
                                                                                                                                                                                                                                                               h 3.9%;
Similarity 52.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid
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Ziai Dr., Mohammad R.
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                                                                            RESULT 13
PCT-US92-06840-1/c
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Best Local Similarity
                                              Sequence 1, Application PC/TUS9206840 GENERAL INFORMATION:
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TELEX: 710-474-4059
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1730 base pairs
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TITLE OF INVENTION:
tent No. 5652111
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/923,095
PRITING DATE: 30-JUL-1992
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ATTORNEY/AGENT INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                    1589 TGGGAGATGCAAGATGAGTACCAGGGGGTGGTTAGGAATAATTTCTAAGTTTTTCCACCT 1648
                                                                                                                                                                                                                                                                                        1529 CCCTTTATGGTGGGCTTTGTTTTTTAAAGCCACGGACAATGGCACAGCTTACCTCAG 1588
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              APPLICANT:
                                                                                                                                                    1649 TGAATGCTGAGTGG 1662
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APPLICANT:
                                                                                                                                                                                                                                                                                                                 343 ccctgtgtggatggctgggtatatgatcaaagctacttcccttcgaccattgtgactaag 402
                                                                                                                                                                                  463 ggaatgctggtggg 476
                                                                                                                                                                                                                                                    403 tgggacctggtatgtgattatcagtcactgaaatcagtggttcaattcctacttctgact 462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 140..1456
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1937 West Main Street
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            Shi, Yang
Seto, Edward
Shenk, Thomas
                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                              64; Indels
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Best Local Similarity
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TELEX: 236925
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2353 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
OStrolenk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 30,623
REFERENCE/DOCKET NUMBER: M-12594 CIP (1570-8)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 382-0700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/746,485
FILING DATE: 16-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
ORGANISM: Hom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                   IMMEDIATE SOURCE:
2153 TTAAATCAC 2145
                                                             2213 CTGGCAGTATTTTTTTGGAAAAAAAAAAGTGACTAAAATGGGTTTAAATTGATTAACACTA 2154
                                                                                                                               2273 ACAACTGAGCACCACTTTCTGTAACTGAACAGGCAAAGAAATTACACTGAACATCAGCAT 2214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE:
                                                                                729 tatoctggtatttttgagaaaaaaatctcaaggaaaaggcataaaaatgattgctacac 788
                                                                                                                                                           669 acagaccaaaactactgtgtgtgacttgttccgcaaccccagtatgcgtaaaaggatctg 728
                             789 aaaagtgac 797
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                  NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                        CELL TYPE: tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE TYPE: HeLa cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (212) 382-0888
                                                                                                                                                                                                                                                                                                                                                       CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                      LIBRARY:
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1180 Avenue of the Americas - 7th Floor
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52.7%;
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RESULT 14

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Chen, Fang
TITLE OF INVENTION: DAM MOLECULES ENCODING HUMAN NUCLEAR
TITLE OF INVENTION: RECEPTOR PROTEINS
FILE REFERENCE: 19999Y
CURRENT APPLICATION NUMBER: US/09/141,000
CURRENT APPLICATION NUMBER: US/09/141,000
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FASTSEQ for Windows Version 3.0
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 458
TYPE: PRT
ORGANISM: Human
US-09-141-000-4
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US-09-141-000-4/c
US-09-141-000-4/c
; Sequence 4, Application US/09141000
; Patent No. 6054295
; Patent No. 6054295
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APPLICANT: Nislow, Corey
APPLICANT: Sakowicz, Roman
APPLICANT: Beraud, Christophe
TITLE OF INVENTION: Antifungal Assay
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 3.9%; Score 31.4; DB 4; Length 3741; Best Local Similarity 57.7%; Pred. No. 4.2; Matches 56; Conservative 0; Mismatches 41; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 1015
CURRENT APPLICATION NUMBER: US/09/541,782
CURRENT FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1193 aaaaatggagtgtatatttotgaagaaaattttagagtcatgagtggaaaattaactgtt 1252
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264 TM.HSH.BA.H.KTR.M...TB..DSB.MNR.MMT..B...N.R.SN.TH.YYMRM.YCC 205
                           215 tettgagaatetetateeeactagaetetaaatetgaggeeagaagatgtegtegetttg 274
                                                                                          324 ..H..S.SYRBBC....KWTS...SK.HT.S.AS.C..DMTWC..BB..YHT.HG.AA. 265
                                                                                                                                        155 acatgctggacaataatactggatctggtaatgaaactggaatcctcagtgaagatgccc 214
                                                                                                                                                                                          384 H..DKSHSNT.T.TM.AB...M..MKSMRMMB....TNN.H..CT.MS.H.HK.RHHTRB 325
                                                                                                                                                                                                                                                                                       444 BMC..M.NR.D.BTMASA.Y....AK.KMCTYY.H.KD.CT.RH..T.D.BH..M.BT.B 385
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Search completed: July 1, 2002, 15:40:20 Job time: 10469 sec

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
387
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Gapop 10.0 , Gapext 1.0
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Listing first 45 summaries
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                                                                    AQ280703 CITBI-E1-
AQ127694 HS_3091_B
AQ280563 CITBI-E1-
AA682573 zj20a06.s
BG566618 602585464
BI338656 362506 MA
AQ237446 RPCII1-69
BG972774 602837672
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	AW012307 um07c06.y	AT315917 u127f05.y	AW107600 ul93a06.y	AI956697 ul75d06.y	BI328477 602985750	AW611026 un75f02.y	BF785293 602108493	AW106794 um33f07.y	AW475431 un66c08.y	BB637428 BB637428	BF788430 602114177	BB661292 BB661292	AW475229 un63c01.y	AW259000 um76b08.y	BI143310 60290/858	AA033971 Z105C09.1	BB66131/ BB60131/	DECC1317 DESC1317	7.563462 11K3305.V	BT332219 602981678	BT763962 603049842	AT316141 u125e04.y	AT746617 ul01d05.y	ထ	AV605334 AV605334	· u	, 4	DECOTED BEASO759	PR654082	) ui88f0

ALIGNMENTS

RESULT AV652088 DEFINITION ACCESSION COMMENT REFERENCE SOURCE KEYWORDS VERSION LOCUS FEATURES ORGANISM JOURNAL AUTHORS source Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W., Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Hu.G., Gu,J., Chen,Z. and Han,Z.
Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver with those of corresponding noncancerous liver with Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001) 615 bp mRNA linear EST 15-JAN-2 AV652088 GLC Homo sapiens cDNA clone GLCCWF10 3', mRNA sequence. Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
S51 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922 Homo sapiens AV652088.1 GI:9873102 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Email: hanzg@chgc.sh.cn This clone is available at CHGC in Shanghai. 21625106 human. (bases 1 to 615) /tissue\_type="corresponding non cancerous liver tissue"
/dev\_stage="Adult"
/lab\_host="SOLR" 1. .615 /organism="Homo sapiens" /db\_xref="taxon:9606" Location/Qualifiers note="Vector: pBluescript sk(-); Site\_1: EcoRI; Site\_2: /clone="GLCCWF10" /clone\_lib="GLC" EST 15-JAN-2002

BASE COUNT

146

Pudong, Shanghai

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RESULT 2
AV699858/c
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                     547 CACTGAAATCAGTGGTTCAATTCCTACTTCTGACTGGAATGCTGGTGGGAGGCATCATAN 606
                                                                                                                                                                                                                                                                                                                                                                                        614 cactgaaatcagtggttcaattcctacttctgactggaatgctggtgggaggcatcatag 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                   554 atcaaagctacttcccttcgaccattgtgactaagtgggacctggtatgtgattatcagt 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           434 tgaggccagagaagtgtcgtcgctttgtccatccccagtggcagcttcttcacctgaatg 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      374 aaactggaatcotcagtgaagatgccctcttgagaatctctatcccactagactcaaatc 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         307 AAACTGGAATCCTCAGTGAAGATGCCCTCTTGAGAATCTCTATCCCACTAGACTCAAATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             194
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                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 779)
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                                                                                                                                              Homo sapiens
                                                                                                                                                                                                              AV699858 GKC Homo sapiens cDNA clone GKCDLE04 3', mRNA sequence.
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Similarity 91.8%;
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1630 gcaaaggccaggttcagcaattttcaaactgtatgtacatttaataaaataactataaat 1689
                                                  1570 attttaaacaaatagctggtatagtttacaatattataaagatattgttcaaattgaagg 1629
                                                                                            JOURNAL
                                                                                                                                                                           1450 aaagattagatactaaataacattgactatctcttttgtaaatacagtcactaaatgatgt 1509
                               170 ATTTTAAACAAATAGCTGGTATAGTTTCCAATATTATAAAGATATTGTTCAAATTGAAGG 111
                                                                                                                                                                                                                                       1390 gacctatataaatgcatttaatacatgatacttttgacataataagccattggaaaacgg 1449
                                                                                                                                                                                                                                                                                   1270 tcacagaattaggatgtggctggctggtgtatgaagcaccatgtgatgaattcataaagt 1329
                                                                                                                                                                                                                                                                                                                                                                                                            290 AAAGATTAGATACTAAATAACATTGACTATCTCTTTGTAAATACAGTCACTAAATGATGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     645 ATATTTTAAA-ACATGAATCCNATTATAATAT----GGCATTATNTGCAATTTATTTCANA 590
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 32.0%; Local Similarity 91.6%;
                                                                                                                                                                                                                        GACCTATATAAATGCATTTAATACATGATACTTTTGACATAATAAGCCATTGGAAAACGG
                                                                                                                                                                                                                                                                                                                                                 TCCCAGAATTAGGATGTGGCTGGCTGGTGTATGAAGCACCATGTGATGAATTCATAAAGT 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             619;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chinese National Human Genome Center at Shanghai 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, 201203, P. R. China Tel: 86-21-50801919(ex.45)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: hanzg@chgc.sh.cn
This clone is available at CHGC in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Zeguang Han
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="GKCDLE04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="SOLR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                   43 TICCCGACGTACGACGTCCGCGGAGCTCTTGAGTCAAGTTGGAGGCCTTCGGAGATTTCA 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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tactggatctggtaatgaaactggaatcctcagtgaagatgccctcttgagaatctctat 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); and Chemical Research (RIKEN), Tokohama, Kanagawa 230-0045, Japan 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp/, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9110, Fax:81-45-503-9170)
Tel:81-45-503-9111, Fax:81-45-503-9170
Tel:81-45-503-9111, Fax:81-45-503-9170
Was generated during the R&D process and may have higher chance of the companion of the R&D process and may have higher chance of the companion of the R&D process and may have higher chance of the companion of the R&D process and may have higher chance of the companion of the R&D process and may have higher chance of the companion of the comp
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Totoki,Y., Watanabe,H. and Sakaki,Y.
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Totoki,Y., Watanabe,H. and Sakaki,Y.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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troglodytes male_lymphoblast DNA, clone_lib:PTB Chimpanzee Male
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R.Site 1 : SacI
R.Site 2 : SacI.
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/clone_lib="PTB Chimpanzee Male BAC Library"
160 c 154 g 207 t 5 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:9598"
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Pred. No. 4.3e-55;
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629 ttcaattcctacttctgactggaatgctggtgggaggcatcataggtggccatgtctcag 688

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                              Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptce,M., Tan,F., Theising,B.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40ml3 fwd. ET from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 399
Conservative
                                                                                                                                                                                                                                                                            constructed by Bento Soares and M. Fatima Bonaldo."
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/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="male"
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                                          22.7%;
99.7%;
           0; Mismatches
                                      Score 387; DB 9; Length 399; Pred. No. 7.3e-55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              219 ACATAGAGGTTGTAAGATCCACCATGCAGGAGGAGCTGGATGCAGCACAGACCAAAACTA 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                809 acatagaggttgtaagatccaccatgcaggaggagctggatgcagcacagaccaaaacta 868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               279 TAAAGGCACTTAGAAAAGTTGCACGCACAAATGGAATAAAGAATGCTGAAGAAACCCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   749 taaaggcacttagaaaagttgcacgcacaaatggaataaagaatgctgaagaaccctga 808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   339 ACAGGTGGCTGGTGGAATCTGCTCGGTGGTTGATAATCACCAATAAACTAGATGAGGGCT 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39 TTTTAAGAAGCCTTCATGAGCTGATTGGTGGGGAAATTC 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGTGTGTGACTTGTTCCGCAACCCCAGTATGCGTAAAAGGATCTGTATCCTGGTATTTT 100
                                                                                                                                                                                                                                                                                                  Contact: Mark Adams
Department of Eukaryottic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                            Seq primer: M13 Reverse Class: BAC ends.
                                                                                                                                                                                                                           http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
                                                                                                                                                                                                                                                            Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
                                                                                                                                                                                                                                                         end search page:
                                                                                                                                                                                                                                                                                                                                                                                                              Other_GSSs: CITBI-E1-2514B2.TF
                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Use of a random human BAC End Sequence Database for Sequence-Ready
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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CITBI-E1-2514B2.TR CITBI-E1 Homo sapiens genomic clone 2514B2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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/clone_lib="CITBI-E1"
/sex="male"
                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2514B2"
                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 TGATGTTAGTTACTTTTCCATGGTGGAATTTTAATTACTTTTTCTTTTGTAATTTTTCTCT 240
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                                                                                                                                                                                                                     High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618 Fax: (206) 616-3887
                                                                                                                                            High quality sequence stop: 474.
                                                                                                                                                            Class: BAC ends
                                                                                                                                                                                          Sequence Tagged Connector
                                                                                                                                                                                                            Email: jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                        Contact: Mahairas GG, Wallace JC, Hood L
                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 474)

Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Hond.T., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                382;
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                                                                                                                                                                                 3091
                          /clone="Plate=3091 Col=4 Row=D"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                           Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and
                                                                                                                                                                     Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                 Use of a random human BAC End Sequence Database for Sequence-Ready
                                               Seq primer: M13 Reverse
Class: BAC ends
                                                                                                  Clones are available from Research Genetics (info@resgen.com). BAC
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                                                                        http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No. 1.6e-52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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zj20a06.sl Soares_fetal_liver_spleen_lNFLS_S1 Homo sapiens cDNA
clone IMAGE:450802 3' similar to TR:G1293672 G1293672
                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 367), Bowles,L., Dubuque,T., Geisel,G., Jost,S., Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin Krizman,D., Kucaba,T., Lacy,M., Steptoe,M., Tan,F., Theising,B., J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                               KIDNEY-SPECIFIC TRANSPORT PROTEIN. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                             AA682573.1 GI:2669854
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Seq primer: -40ml3 fwd. ET from Amersham
                                                                                                                                                                     Unpublished (1997)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                             human
                                                                                                                             Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                         Tel: 314 286 1800
Fax: 314 286 1810
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a 79 c 88 g 182 t
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/clone_lib="CITBI-E1"
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/note="vector: pBel
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98.5%;
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Pred. No. 4.4e-52;
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               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 754)
                                                                                                                           Homo sapiens
                                                                                                                                                                                                        602585464F1 NIH_MGC_76 Homo sapiens cDNA clone IMAGE:4714598 5
                                                                                                                                                                         BG566618.1 GI:13574271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
This is a subtracted version of the original Soares fetal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Soares_fetal_liver_spleen_lNFLS_S1"
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/db_xref="taxon:9606"
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                543 ctgggtatatgatcaaagctacttcccttcgaccattgtgactaagtgggacctggtatg 602
627 CTGGGTGTTTGACAGAATCTCCTTCTCATCCAACATCGTGACTGAGTGGGATCTGGTATG 686
                                                                                        484 cacctgaatgggactatccacagcacaagtgaggcagacacagaaccctgtgtgg-atgg 542
                                                                   567 CACCTGAATGGGACCTTCCCCCAACACAAGTGACGCAGACATGGAGCCCTGTGTGGGAATGG
                                                                                                                                     507 GACTCAAACATGAGGCCAGAGAAGTGTCGTCGCTTTGTTCATCCTCAGTGGCAGCTCCTT 566
                                                                                                                                                          424 gactcaaatctgaggccagagagtgtcgtcgtcgctttgtccatccccagtggcagcttctt 483
                                                                                                                                                                                                          447 TCTGACAATGACACTGGGGCCCTCAGCCAAGATGCACTCTTGAGAATCTCCCATCCCACTG 506
                                                                                                                                                                                                                             364 totggtaatgaaactggaatcotcagtgaagatgccotottgagaatctotatcccacta 423
                                                                                                                                                                                                                                                                              387 TTCACTGCATTCATACCTGGCCATCGCTGCGTGCACACTCCTGGGACAATGACACTGTC 446
                                                                                                                                                                                                                                                                                                   304 tttgctgcagccattcctggtcatcgttgctgggtccacatgctggacaataatactgga 363
                                                                                                                                                                                                                                                                                                                                                327 CAGACTGTTTTTCTCTCAATCTTTGCTGTTGCTACATACCTTCATTTTATGCTGGAGAAC 386
                                                                                                                                                                                                                                                                                                                                                                                 244 catctggtttttattcttccctctctcatgttattaatccctcatatactgctagagaac 303
                                                                                                                                                                                                                                                                                                                                                                                                                                          184 tcaatggcctttgaggagctcttgagtcaagttggaggccttgggagatttcagatgctt 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         207 CTCTTTGAACCTCTCTGGATACAGTCATTTTGCCTCTACTTGAGGATCAACTGTTCAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 ccctttgaacttatctccgtaaagccattgtgcctcctcttgggggtcacgtgttcacaa 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 agaaattgatgcgaggatcaatacaagcttaatttgaattaataaaaggaaatattttct 123
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                                                                                                                                                                                                                                                                                                                                                                                                                   TCAATGGCCTTTCAGGACCTCCTGGGTCACGCTGGTGACCTGTGGAGATTCCAGATCCTT 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics Inc.
Clone distribution: MGC clone distribution information can be http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence
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/Clone_Ilb="NHI MGC_T/6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        745 GAGGCATC 752
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      603 tga-ttatcagtcactgaaatcagtggttcaattcctacttctgactggaatgctggtgg 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
                                                                                                                                                                                                                                        111 ggaaatattttctccctttgaacttatctccgtaaagccattgtgcctcctcttgggggt 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10
                                                                                                                                                     171 cacgtgttcacaatcaatggcctttgaggagctcttgagtcaagttggaggccttgggag 230
291 actgctagagaactttgctgcagccattcctggtcatcgttgctgggtccacatgctgga 350
                                                                                         231 atttcagatgcttcatctggtttttattcttccctctctcatgttattaatccctcatat 290
                                                                                                                               57 CACCTGTTCA----CAATGGCTTTTGAGGAGCTCCTGAATGAAGTCGGTGGCTTGGGGAA 112
                                                                                                                                                                                                        1 GAAAACTTTTTCTCCCTTTGA----CTTACTTATAAATCCATGTGACTCCTCTTGAGGAC 56
                                                       362506 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
BI338656
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Sus scrofa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390 Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST discovery in swine Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Design and use of two pooled tissue normalized cDNA libraries for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fahrenkrug, S.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plate: 131 row: H column: 23 Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BACKWARD: GTTTTCCCAGTCACGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FORWARD: AGGAAACAGCTATGACCAT
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Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from day 11, 13, 15, 20, and 30 embryos."

163 c 136 g 159 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:9823"
/clone_lib="MARC 1PIG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Sus scrofa"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="DH10B"
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                                                                                                                                                                                                                                                                                    19.3%; Score 328.8; DB 10; Length 75.2%; Pred. No. 3.1e-45; Ative 0; Mismatches 137; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 741)

1 (bases 1 to 741)

1 Adams, M. D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C. Use of human BAC End Sequences for Sequence-Ready Map Building Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7911 Medical Center Dr., Rockville, MD 20850, USA
7e1: 301 838 0200
Fax: 301 83 0200
Fax: 301 83 0208
Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the contact Pieter de Jong
library availability, please Contact P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   primer:
                                         /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11_Human Male BAC Library"
                                                                                                                                                                                                   /db_xref="taxon:9606"
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/clone_lib="RPCI-11"
                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="GDB:7526365"
                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                              /sex="Male"
                156 c
                188 g
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source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       237 CTGGGTGTATGACAGAATCTCCTTCTCATCCACCATCGTGACTGAG 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183 atcaatggcctttgaggagctcttgagtcaagttggaggccttgggagatttcagatgct 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          657 CCTCTTTGAACCTCTCTGGATACAGTCATTTTGCCTCTACTTGAGGATCAACTGTTCAAC 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123 tccctttgaacttatctccgtaaagccattgtgcctcctcttgggggtcacgtgttcaca 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    717 AGAGAGTGGGTTCAGGATCAAAACACATTTAGTGTGACTTAGGGGAAAAGAAAAACATTTTC 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 agaaattgatgcgaggatcaatacaagcttaatttgaatta-ataaaagggaatattttc 122
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                                                                                                          Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTCAATGGCCTTTCAGGACCTCATGGGTCACGCTGGTGACCTGTGGAGATTCCAGATCCT
      High quality sequence start: 13
High quality sequence stop: 819,
Location/Qualifiers
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                                                         found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM10958 row: o column: 18
                                                                                                                                                                                                                                                                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                               Unpublished (1999
                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Muses 1 to 820)
                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
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Similarity 76.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                 640 cttctgactggaatgctggtgggaggcatcataggtgggccatgtctcagacaggt 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        572 GTGACTGAGTGGGACCTGGTGTGTGAATCTCAGGCACTGAATTCTGTTGCTAAATTTTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    460 gtccatccccagtggcagcttcttcacctgaatgggactatccaccagcaccagtgaggca 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          392 CTCCTGAGGATCTCCATCCCCCTGGATTCCAACCTGAGACTGGATAAATGTCGTCGTTTT 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      332 CCCATCCTTGACAATGACACTGCCTCTGATAATGGCAGTAGGATCCTGAGCCAAGATGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 340 cacatgctggacaataatactggatctggtaatgaaactggaatcctcagtgaagatgcc 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      272 GTACCTCATATTACAATGGAGAACTTTACTGCAGCCATTCCCCAATCATCGCTGCTGGGCC 331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  212 AGCCTAGGAAGATTCCAGATCCTTCAGATCTCTTTTGTTCTCTTCCTCGTAGGCCTTGTG 271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             152 CCCATCGGAGATAGTCATTCAGTTCCAATGGCCTTTCAGGAACTCCTGAATCAAGTTGGA 211
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                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 866)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                             EST
                                                                                                                                                                                                                          BI102429.1 GI:14553322
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602889616F1 NCI_CGAP_Kidl4 Mus musculus cDNA clone IMAGE:5044850
5', mRNA seguence.
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/clone=lib="NCI_CGAP_Kid14"
/clone_lib="NCI_CGAP_Kid14"
/lab_host="DH10B (T1 phage=resistant)"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sali; Cloned unidirectionally. Primer: Oligo dT
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. | "
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/strain="FVB/N"
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72.3%;
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Pred. No. 3.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTCCTGAGGATCTCCATCCCCTGGATTCCAACCTGAGACTGGATAAATGTCGTCGTTTT 445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCCCAACCACAGTGGCATCTTCTTCATTTGAATGGCACTTTCTCCAATGAGACAGAGCCA 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cacatgctggacaataatactggatctggtaatgaaactggaatcctcagtgaagatgcc
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                                                                                                                                                                                                                                       cttctgactggaatgctggtgggaggcatcataggtggccatgtctcagacaggtgg 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCCATCCTTGACAATGACACTGCCTCTGATAATGGCAGTAGGATCCTGAGCCAAGATGAC
                                                                                                                                                                                                              ATTCATGATTGGCTATTTATAGGGGGCTATCATATGTGGCCATTTGTCAGACAGGTTG 682
                                                                                                                                                                                                                                                                                                          GTGACTGAGTGGGACCTGGTGTGTGAATCTCAGGCACTGAATTCTGTTGCTAAAATTTTC 625
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://image.llnl.gov
Plate: LLAM11122 row: p column: 03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              found through the I.M.A.G.E. Consortium/LLNL at:
                                     AW107114 739 bp mRNA linear Lot 20 001 um18h07.yl Sugano mouse kidney mkia Mus muscullus cDNA clone IMAGE:2192701 5' similar to TR:070609 070609 PUTATIVE INTEGRAL
AW107114
                   MEMBRANE TRANSPORT PROTEIN. ; , mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. |"
a 206 c 189 g 268 t 1 others
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/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5044850"
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71.7%;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                  160 ctcttgggggtcacgtgttcacaatcaatggcctttgaggagctcttgagtcaagttgga 219
380 CCCATCCTTGACAATGACACTGCCTCTGATAATGGCAGTAGGATACTGAGCCAAGATGAC
                              340 cacatgctggacaataatactggatctggtaatgaaactggaatcctcagtgaagatgcc 399
                                                                                                         320 GTACCACATATTGGAATGGAGAACTTTACTGCAGCCATTCCCAATCATCGCTGCTGGGTC
                                                                                                                                                                                                              260 AGCCTAGGAAGATTCCAGATCCTTCAGATAGTTTTTCTTTTCCTCCTCAATGCCATTGTA 319
                                                                                                                                                                                                                                                           220 ggccttgggagatttcagatgcttcatctggtttttattcttccctctctcatgttatta 279
                                                                                                                                                                                                                                                                                                                     200 CCCTTTGGAAATAGTTATTCAACCTCAATGTCCTTTCAAGAACTCCTGAATCAAGTTGGA 259
                                                                                                                                atcoctcatatactgctagagaactttgctgcagccattcctggtcatcgttgctgggtc 339
                                                                                                                                                                                                                                                                                                                                                                                                                               382;
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The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AW107114.1
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGI:1005153
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                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Organ: kidney: Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed with an oligo(dT) primer [ATGTGGCTTTTTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested and cloned into distinct DraIII site CACCATGTG, 3 site CACCATGTG, XhoI shoul be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            primer CGACCTGCAGCTCGAGCACA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:10000"
/clone="IMAGE:2192701"
/clone_lib="Sugano mouse kidney mkia"
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/lab_host="DH10B"
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu
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71.4%;
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248 tggtttttattcttccctctctcatgttattaatccctcatatactgctagagaactttg 30
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                                                                  tggcctttgaggagctcttgagtcaagttggaggccttgggagatttcagatgcttcatc 247
                                          TGGCCTTTCAGGAACTCCTGAATCAAGTTGGAAGCCTAGGAAGATTCCAGATCCTTCAGA 60
                                                                                                                                  373;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM9848 row: d column: 18
High quality sequence stop: 665.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M. E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 to 1054)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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5', mRNA sequence.
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Clone distribution: MGC clone distribution information can be
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Site_2: Sall; Cloned unidirectionally. Primer: Oli.
Site_2: Sall; Cloned unidirectionally. Primer: Oli.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. | "
a 250 c 256 g 272 t
                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
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                                                                                                                                                   17.2%;
73.6%;
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                                                                                                                           Score 292.6; DB 10;
Pred. No. 2.7e-39;
0; Mismatches 134;
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                | tcataggtggccatgtctcagacaggt 694
                                                         CTCAGGCACTGAATTCTGTTGCTAAATTTTCATTCATGATTGGCCTATTTATAGGGGGCTA 480
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Search completed: July 1, 2002, 14:44:55 Job time: 9394 sec

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Maximum DB seq length: 2000000000
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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nucleic search, using sw model
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1: /cgn2_6/ptodata/2/
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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     sequence 36, Appli
Sequence 2, Appli
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Sequence 8, Appli
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Sequence 1137, App
Sequence 32, Appl
Sequence 11, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 11, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 937, Appl
Sequence 683, Appl
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Sequence 2, Appli
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Sequence 13, Appli
Sequence 5, Appli
Sequence 541, Appl
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Sequence 2, Appli
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y 70.1 y 70.1 y 70.1 rvative ctccgta             tacgtg ttacgtg ttacgtg tttccttcc       tttcttcc       tttcttcc         tttcttcc	ion US/09172 , Mary Jane Gary B. Scott R. , Jeffrey J. MONITORING: 011 US 11 US 11 198-10-13 5: 61 1 ram 1700607713H1		834 731 1422 2334 837 6243 782 1519 9636 9636 9636 2058 2058 2058 2448 2448	732
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nd. No. 2.9e-16; Add. No. 2.9e-16; Mismatches 67; Mismatches 67; L-gtgcctcctcttggg	172711 ne ig TOXICOLOGICAL RESPONS 75/09/172,711 .13	ALIGNMENTS	US-08-998-416-305 US-08-451-4058-2 US-08-451-4058-2 US-08-62-632-4 US-08-062-632-4 US-08-998-416-288 US-09-007-119-15 US-09-007-119-15 US-09-007-119-15 US-08-323-1708-1 US-08-323-1708-1 US-08-34-441-1 US-08-749-391-1 US-08-749-391-1 US-08-749-391-1 US-08-749-391-1 US-08-749-391-1 US-08-749-391-1 US-08-749-391-1 US-08-749-391-1 US-08-749-720-1 US-08-946-617-2 US-08-946-617-2 US-09-031-897-2 US-09-031-897-2 US-09-031-897-2	US-08-998-416-1036 US-08-998-416-538
Indels 2; Gaps gtcacgtgttcacaat 184			(0 (0 (0 (0 (0 (0 (0 (0 (0 (0 (0 (0 (0 (	e 100

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RESULT 2
US-08-232-463-14/c
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:

APPLICANT:

SCHEIFLINGER, F. DORNER, F.

APPLICANT:

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US-08-232-463-14
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INFORMATION FOR SEQ ID NO:
                                                                                                                        952 aggcataaaaatgattgctacacaaaagtgaccaaattttaagaagccttcatgagctga 1011
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                               652 atgctggtgggaggcatcataggtggccatgtctcagacaggtggctggtggaatctgct 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE:
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APPLICATION NUMBER: 1
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MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                               y Match
Local Similarity 8.7%; Score 60.4; DB 1; Length 7218;
Local Similarity 8.7%; Pred. No. 6.5e-06;
hes 40; Conservative 228; Mismatches 194; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
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ZIP: 22313-0299
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US-07-867-106-2
                                                                 Query Match 3.2%;
Best Local Similarity 49.1%;
                                                       Matches 173;
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                                                                                                                                                                                   FEATURE:
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                                                                                                                                                                                                                                           ANTI-SENSE:
                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US
FILING DATE: 19920625
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5389526ris
STREET: One Liberty Place 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Slade, Martin B
APPLICANT: Chang, Andy C M
APPLICANT: Williams, Keith L
TITLE OF INVENTION: Improved Plasmid Vectors for Cellular
TITLE OF INVENTION: Slime Moulds of the Genus Dictyostellum
                                                                                                                                                                                              NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1049 CCTGCAGCCAAGCTCGGAATTAATTCTGTGAGCGTATGGCAA 1008
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                                                                                                                                                                 NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: AU PJ 7187
APPLICATION NUMBER: PCT/AU90/00530
                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                  0;
                                                            Score 54; DB 1;
Pred. No. 0.00025;
                                          Mismatches 175; Indels
                                                                          DB 1; Length 5852;
                                         4; Gaps
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                                                                           US-08-647-397-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5491 TTTTAAGATTTTTAATCTCGTCAATGATTTTAAAATAAAATCGATACATAATTTTAAA 5550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1525 ggtggaattttaattactttttctttgtaatttttctctctgtatattttaaacaaatag 1584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.1%; Score 53.2; DB 2; Length 2102; Best Local Similarity 56.5%; Pred: No. 0.00026; Matches 122; Conservative 0: Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1585 ctggtatagtttacaatattataaagatattgttcaaattgaagggcaaaggccaggttc 1644
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INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: OSTEOCLAST TRANSPORTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Beier, David R. APPLICANT: Brady, Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Gates, Edward R.
REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                          MOLECULE TYPE: CL
                                                                                                                                                                                         HYPOTHETICAL:
                                                                                                                      FEATURE:
                                                                                                                                                ORIGINAL SOURCE:
                                                                                                                                                                             ANTI-SENSE:
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                                                                                                                                                               RAGMENT TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                          NAME/KEY:
                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                 STRANDEDNESS: double
                                                                                                                                  ORGANISM: Mus musculus
                                                                                                                                                                                                                                                              LENGTH:
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                                                                                                                                                                                                                                                               2102 base pairs
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PE: internal
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SYSTEM: PC-DOS/MS-DOS
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US-08-487-826B-13
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                                                        Matches 217; Conservative
                                                                        Query Match
Best Local Similarity
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APPLICANT:
APPLICANT:
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INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  349 TGCATCTGCCAAACGCCAGTCTTCCCAATGACACCCAGGGGGCCACCGAGCCATGCTTGG 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       539 atggctgggtatatgatcaaagctacttcccttcgaccattgtgactaagtgggacctgg 598
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               599 tatytyattatcaytcactyaaatcaytyyttcaattcctacttctyactyyaatyctyy 658
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     523 TTGGAGGACCTGTGTTTGGAGAACTGTCAGACAGGT 558
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                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: NI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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              1021 aaattcagaaaaaaaaatacaggaaaagaacaccagaagggtttttttccctacaacc 1080
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                                                                                                                                                                                MOLECULE TYPE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                 NAME:
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Miller, Louis
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                                                                             2.9%; Score 49.6; DB 2; Length 19124; 43.8%; Pred. No. 0.0054;
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                                                                                                                                                                                                                                                                                                                                                    29,655
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                                                                0; Mismatches 279;
                                                                        Indels
                                                                           0; Gaps
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RESULT 6
US-08-731-722-5
; Sequence 5, Application US/08731722
; Patent No. 5961971
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                                                  TELEFAX: 352-372-5800
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1186 base pairs
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APPLICANT: Martin,
     MOLECULE TYPE:
                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15961 AAAATTAATTACATGC 15976
                                                                                                                                                              ATTORNEY/AGENT INFORMATION: NAME: Whitlock, Ted W.
                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIIM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TITLE OF INVENTION: Biocont.
TITLE OF INVENTION: by Pyth.
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                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                    REGISTRATION NUMBER:
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                                                                                                                                                                                             CLASSIFICATION:
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                                                                                                                                                                                                                                                       SOFTWARE:
                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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STREET: 2421 N.W. 41st Street, Suite A-1
                                       nucleic acid
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DNA (genomic)
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US-08-998-416-541/c
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                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                            APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.9%;
Best Local Similarity 45.7%;
Matches 290; Conservation
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APPLICANT:
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ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                              750 ATATCTTTAAAAAGATATAAATTAATTACATAAT 783
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      578 ATAAGAAATTCTTCAATAGAGAAAGGTTTTATTTTTCAATAGAAAATTGTAATTCTTAT 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1364 gaaatcaaaataaatccagaaatagagacctatataaatgcatttaatacatgatacttt 1423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           518 ATATTTTAAATAATGATCTGGATTTATACAGTAGATCCTATAAATCTTTAATAGTAGTT 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1184 totgatattttttgggaagtootttaaaaagttacaaatttatoaataaattaotagtaga 1243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1124 ggcattaatttgcattttatttcaaaattaacttgtggggacatgtaatctcttgagcaa 1183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 458 AAAATGAAAATACTTCTAATAAGAATATATTTATTATAAATATTGAAAAACTTTTATTT 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1064 ttttttccctacaaccagcaagaacatatattagatacatgaatctcaattataattat 1123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     342 GCACCTGCTAATCCAATAGTAGCTAATCCAGCACCAATAAATTTTGCAGATTGT-AATAA 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 282 AGAAGGGTTTCTAGAAATACCTAAACTAATGAACTAAATACTGAACCGATACCGATACCA 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     222 AGCAATAGATTCAGTTAAAGCGAAACCTAAAATAGCTGTTCTTGTTAAATCTTGTTGTAA 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            162 TTTTATTAACTTAAATTAAAAAGCGAATAAAATTAAGAAAGCAATCATTAAACAGAATAA 221
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                                                                                                                                                                                                Philippsen, Peter Pohlmann, Rainer Steiner, Sabine
                                                                                                                                            Wendland, Jurgen
Knechtle, Philipp
                                                                                                                                                                                   Mohr, Christine
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Pred. No. 0.0027;
0; Mismatches 332; Indels 12
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US-08-998-416-541
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PRIOR APPLICATION NUMBER: CH 0016/9:
APPLICATION NUMBER: CH 0016/9:
APPLICATION NUMBER: CH 0016/9:
APPLICATION NUMBER: CH 0016/9:
ATTORNEY/ACENT INFORMATION:
ATTORNEY/ACENT INFORMATION:
REGISTRATION NUMBER: PF/5
REGISTRATION NUMBER: PF/5
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEPHONE: 919-541-8689
TELEPHONE: 919-541-8689
TELEPHONE: OF SEO ID NO: 541:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHAR
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                                                                                                                                                                                                                                                      US-08-883-795A-36
Sequence 36, Application US/08883795A
Patent No. 5985607
Patent No. SPECTON:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
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ORIGINAL SOURCE:
ORGANISM: PAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               672 AATNANAATACTTATTATATATTTCATTAATAATATTAAATNTNTTAAAAAATAATTATAA 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      732 AAGGGTAANTNTAAATGCAAATTATTATTAGGGGTCGTTTTNTCATTTTTTTATTATTATNA 673
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APPLICANT: Awang, Gregor
APPLICANT: Awang, Gregor
TITLE OF INVENTION: Recombinant DNA Molecules and Expression
TITLE OF INVENTION: Vectors for Tissue Plasminogen Activator
TITLE OF INVENTION: 99
NUMBER OF SEQUENCES: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       492 TTAAATTATAATTTAAATTT 473
                                                                                  CORRESPONDENCE ADDRESS:
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                             STREET:
                                                           ADDRESSEE:
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Toronto
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31-DEC-1996
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                             E: BERESKIN & PARR
40 King Street West
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IMMEDIATE SOURCE:
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US-08-883-795A-36
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                        В
                                                                                                                   US-08-451-405A-2
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CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
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                                                                                      sequence 2, Application US/08451405A Patent No. 5736358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1367 atcaaaataaatccagaaatagagacctatataaatgcatttaatacatgatacttttga 1426
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REGISTRATION NUMBER: 40,2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/0
FILING DATE: 27-JUN-1997
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                                                                              GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                      1545 ttotttgtaatttttotototgtatattttaaacaaatagotggtatagtttacaatatt 1604
                                                                                                                                                                                                                                                                                                                                                           1487 taaatacagtcact--aaatgatgttagttacttttccatggtggaattttaattacttt 1544
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                                                                                                                                                                                                                                                   1605 ataaagatattgttcaaattgaagggcaaaggccaggttcagcaattttcaaactgtatg 1664
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                                                                                                                                                                                                                                                                                                                                    1665 tacatttaataaaataactataaattaaaaattatattt 1704
                                                                                                                                                                                                                                                                                                                                                                                                                                             266 ATAATTAAAATGTTTATAATTAA----ATATTTTATAATTAAAATGTTTATAATTACATA 321
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APPLICANT: REYMOND, CHRISTOPHE DOMINIQUE
TITLE OF INVENTION: DICTYOSTELID EXPRESSION VECTOR AND
TITLE OF INVENTION: METHOD FOR EXPRESSING A DESIRED PROTEIN
NUMBER OF SEQUENCES: 3
                                                                                                                                                                        322 TITTATAATTAAAAGTTTATAATTACATATTTATAATT 361
CORRESPONDENCE ADDRESS:
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RESULT 10
US-07-867-106-2/c
Patent No. 335322.

GENERAL INFORMATION:
GENERAL INFORMATION:
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APPLICANT:
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                1533 tttaattacttttctttgtaatttttctct 1563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 ATTTTTGTGTTCTTATAATTTGGTTAAATCGATGAATAATATTTGATTAGTATATGTTTT 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISK
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2.6%; Score 44.6; DB 1; Length 731;
Local Similarity 43.7%; Pred. No. 0.026;
Les 197; Conservative 0; Mismatches 254; Indels 0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEIC ACID
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PENNSYLVANIA
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', NAME/KEY: CDS
', LOCATION: 2378..5038
US-07-867-106-2
                                                                                                                                                                                                                                                                                                                                                    Query Match 2.6%; Score 44; DB 1; Length 5852; Best Local Similarity 49.7%; Pred. No. 0.088; Matches 196; Conservative 0; Mismatches 190; Indels
1492 acagtcactaaa--tgatgttagttacttttccatggtggaattttaattactttttctt 1549
                                                       1432 taagccattggaaaacggaaagattagatactaaataacattgactatctctttgtaaat 1491
                                                                                                               2199 AATAAATATAATTAAAATTGTCATGCCAAAACTGATAAATATTTGATATATTATCCAATA 2140
                                                                                                                                  2259 АЛАЛАТАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАТТТТАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАТТАЛТСАЛАЛ 2200
                                                                                                                                                                                              1312 gtgatgaattcataaagttgcaaaagtcaaaacaatactgtacatgcaaccagaaatcaa 1371
                                                                                                                                                                                                                                               1192 ttttgggaagtcctttaaaaagttaccaaatttatcaataaattactagtagatgagatga 1251
                                                                                                                                                                                                                            2318 AT-TTACAATAAATAAAATAAAATAAAATGAAAGTGTGGGGAAAAATAAAAATTAAAAATT 2260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/07/867,106
FILING DATE: 1920625
FILING DATE: 1920625
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU DJ 7187
FILING DATE: 02-NOV-1989
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 35,134
FELECOMMUNICATION INFORMATION:
REGISTRATION NUMBER: 35,134
FELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEPHONE: 215-568-3100
TELEPHONE: 215-568-3439
                                                                                                                                                                                                                                                                                    FEATURE:
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INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-TOOS/MS-DOS
SOFTWARE: Patentin Release #1.0, v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 5852 base pairs
TYPE: NUCLEIC ACID
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5389526ris
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CITY: Philadelphia
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2378..5038
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1550 tgtaatttttctctctgtatatttttaaacaaata 1583

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RESULT 11
US-08-883-795A-36/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 665 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Delcuve, Genevieve
APPLICANT: Awang, Gregor
TITLE OF INVENTION: Recombinant DNA Molecules and Expression
TITLE OF INVENTION: Vectors for Tissue Plasminogen Activator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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FILING DATE: 27-JUN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: GRAVELLE, Micheline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                 1315 atgaattcataaagttgcaaaagtcaaaacaatactgtacatgcaaccagaaatcaaaat 1374
                                                                                                                                                                                                                                                                                                                                                                                                                                   IMMEDIATE SOURCE:
CLONE: Rh 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                            1375 aaatccagaaatagagacctatataaatgcatttaatacatgatacttttgacataata- 1433
1554 attittetetetgtatatitttaaacaaatagetggtatagtitaeaatattataaagata 1613
                                                                                                                                        1434 agccattggaaaacggaaagattagatactaaataacattgactatctctttgtaaatac 1493
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                                                                   1494 agtcactaaatgatgttagttacttttccatggtggaattttaattactttttctttgta 1553
                                                                                                                                                                                                                                                 410 ATGTAATTATAAACATTTTAATTATAAAATATGTAATTATAAACATTTTAATTATAAAAT 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Gravelle, MICHELLIE REGISTRATION NUMBER: 40,261
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                                                                                                                                                                            350 ATGTAATTATAAACATTTTAATTATAAAATATGTAATTATAAACATTTTAATTATAAAAT 291
                                  y Match 2.6%;
Local Similarity 47.9%;
nes 186; Conservative
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                                                                                                                                                                                                                                                                                                                            ; Score 43.6; DB 2; Length 665; pred. No. 0.045; 0; Mismatches 199; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-07-991-867B-8
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APPLICANT: Moyer, F
APPLICANT: Hall, Ri
APPLICANT: Gruidl,
US-07-991-867B-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1674 taaaataactataaattaaaaaattata 1701
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ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 5476781el Entomopoxvirus Expression System
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 92/14818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 30-JAN-
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
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                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                       FEATURE:
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COMBITTER: IBM PC compatible

COMBITTER: THE PC COMPANIENT OF THE 
                                                                                                                                                                                           FEATURE:
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                                                                                                  FEATURE
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                                                                                                                                 LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1511 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                     unknown
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US-08-107-755A-8
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Patent No. 5721352
                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                              APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 5721352el Entomopoxvirus Expression System
CORRESPONDENCE ADDRESS:
ADDRESSE, Date 12.5.
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                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                     SOFTWARE:
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                                                                                                    COUNTRY: U
ZIP: 32606
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                                                                                                                                       STATE:
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STREET: 2421 N.W. 41st Street, Suite A-1
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        PatentIn Release #1.0, Version #1.25
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US-08-107-755A-8
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Best Local Similarity
1232 AAAAAATTAATAATATCTAAAAATAAATTTGGTAACTTTAATAATGTTTTTCCTATTAG 1291
                   1496 toactaaatgatgttagttacttttccatggtggaattttaattactttttctttgtaat 1555
                                                                      1176 AATTGTGAATCATGTAATATAAATGACTATA----ATTTTATTAATAATTTAGTAAATTT 1231
                                                                                                      1436 ccattggaaaacggaaagattagatactaaataacattgactatctctttgtaaatacag 1495
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INFORMATION FOR SEQ ID NO:
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NAME/KEY:
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ORIGINAL SOURCE:
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LENGTH: 1511 base pairs
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TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US 0:
FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
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45.5%; Pred. No. 0.063;
Tative 0; Mismatches 324; Indels 14; Gaps
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                                                                                                                                     INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS: LENGTH: 1511 base pairs
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                                                      MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 0:
FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENCEN, GETARD H.
                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
FILING DATE: 30-JAN-
PRIOR APPLICATION DATA:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Gerard H. Bencen
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 5935777el Entomopoxvirus Expression System
NUMBER OF SEQUENCES: 77
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NAME/KEY: CDS
                           ORGANISM: Amsacta moorei entemopoxvirus
                                                                                       TOPOLOGY:
                                                                                                          STRANDEDNESS:
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                                                                                                                                                                                                                                                                   NAME: Bencen, Gerard H. REGISTRATION NUMBER: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: WO 92/14818 FILING DATE: 12-FEB-1992
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FILING DATE: 19-AUG-1993
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                                                                                                    nucleic acid
EDNESS: double
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                                                               DNA (genomic)
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US-08-998-416-1137/c

Sequence 1137, Application US/08998416 Patent No. 6239264

GENERAL INFORMATION:

APPLICANT: Rebischung, Corinne TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII TITLE OF INVENTION: AND USES THEREOF

APPLICANT: APPLICANT: APPLICANT: APPLICANT:

Wendland, Jurgen Knechtle, Philipp Pohlmann, Rainer Steiner, Sabine Mohr, Christine Philippsen, Peter

APPLICANT:

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1412 AAAATTTCCAAAAAGTATAA 1431
                                    1675 aaaataactataaattaaaa 1694
                                                                    1616 gttcaaattgaagggcaaag-gccaggttcagcaattttcaaactgtatgtacatttaat 1674
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/998,41
FILING DATE: 24 DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31 DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 1137:
SEQUENCE CHARACTERISTICS:
LENGTH: 636 base pairs
TYPE: nucleic acid
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
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CITY: Research Triangle Park
STATE: No. 6239264th Carolina
1560 ctctctgtatattttaaacaaatagctggtatagtttacaatattataaagatattgttc 1619
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ZIP: 27709
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                                                     246 TAATAACTAATTTAAAATTTGAACATAGACTAAATAGTATTCATATTAAATATTATTTT 187
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Db 126 GTATTAATAATCAAATAATTAATTT 102

Search completed: July 1, 2002, 15:40:48 Job time: 10497 sec

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OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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773
761
759.4
738.6
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N_GIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1981.DAT:*
2: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1981.DAT:*
2: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1982.DAT:*
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5: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1985.DAT:*
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7: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1986.DAT:*
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Listing first 45 summaries
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98JP-0119395	99WO-JP02226			Location/ 187993 /*tag= a /product=		nbrane ( cansport) c; prime ist; li	ne protein	st entry)		l; cDNA;		1977 22455 2455 2455 2465 24047 22194 2219 540 540 540 540 540 540 540 1871 1871 1871 1871 1871 1871 1871 187
.939	1222			η/ου 3 a t='		doma ter; er; gand	tein	SY)		1705		
				Location/Qualifiers 187993 /*tag= a /product= "Human transmembrane		HP02000; transmembrane domain; liver; expression; organic cation transporter; drug excretion; antib diagnostic marker; primer; probe; antisense; gene agonist; antagonist; ligand; therapeutic; ds.	CDNA clone HP02000			)5 BP.	ALIGNMENTS	AAC85823 AAC85823 AAD17476 AAD17476 AAD17480 AAD12607 AAP32614 ABA30394 AAK11579 AAK37346 AAL118174 AAL07074 AAL07074 AAL07075 AAL07075 AAL07075 AAL07075 AAL07075 AAL07076 AAK24178 AAL07075 AAL07096 AAK24178 AAL07096 AAK24178 AAL07096 AAK24178 AAL07096 AAK24178 AAL07096 AAK24178 AAL07096 AAK33334 AAL07096 AAK93334 AAL07096 AAK93334 AAL07096 AAK93334 AAL07096 AAK93334 AAL07096 AAK93334 AAL07096 AAL07
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Best Local (
                  541
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                                                                                                                         481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents the human cDNA clone HP02000 which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4; Page 89-91; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human proteins with transmembrane domains, involved in control of cell proliferation and differentiation, useful for treating e.g. cancer or
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tomatt; monkey; dog; sea urchin; expressed sequence tag; EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human EST-derived coding sequence SEQ ID NO: 704.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diagnostics; forensic test; gene mapping; genetic disorder; biodiversity; gene therapy; nutrition; ss.
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17-JUL-2000; 2000US-0617746.
03-AUG-2000; 2000US-0631451.
15-SEP-2000; 2000US-0663870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200154477-A2
                                                                                                                                                                                                                                                                         The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a cDNA biodiversity and for nutritional purposes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 638; 1275pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated polypeptide for treatment of diseases, diagnostics, raising antibodies and research use \mbox{\ensuremath{^{\circ}}}
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vA, Zhang
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Pred. No. 1.7e-218;
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09-FEB-2000 (first entry)

HP02000; transmembrane domain; liver; expression; homology; Human transmembrane protein cDNA clone HP02000 coding sequence. AAZ38316

AAZ38316 standard; cDNA; 804 BP

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This sequence represents the coding sequence of human cDNA clone CPMA which encodes a 32 kD protein with two putative transmembrane domains. The cDNA was isolated from a human liver cell cDNA library, and the community of the liver. The protein has been found to be expressed only in transporter (EMBL Accession No. V0945) which is involved in drug cextrection, and may have a similar function. The protein GC may be used to raise specific antibodies, as assay reagents, as CC ligands and binding proteins, and as binding proteins, and as binding active agents. CC Nucleotides encoding the protein may be used as primers and probes or CC antisense molecules, and in gene therapy. Cells transformed with these CC potentially useful therapeutically.
                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                   427
                                                   181
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 804 BP; 226 A; 171 C; 193 G; 214 T; 0 other;
                                                                                                                    121
                                                                                                                                                                                                                                                  187 atggcctttgaggagctcttgagtcaagttggaggccttgggagatttcagatgcttcat 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; Page 84; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human proteins with transmembrane domains, involved in control of cell proliferation and differentiation, useful for treating e.g. cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-023358/02.
P-PSDB; AAY52386.
                                                                                                                                                                                   61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organic cation transporter; drug excretion; antibody; assay reagent; diagnostic marker; primer; probe; antisense; gene therapy; agonist; antagonist; ligand; therapeutic; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PROT-) PROTEGENE INC
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tcaaatctgaggccagagaagtgtcgtcgctttgtccatccccagtggcagcttcttcac
                               99taatgaaactggaatcctcagtgaagatgccctcttgagaatctctatcccactagac
                                                 ggtaatgaaactggaatcctcagtgaagatgccctcttgagaatctctatatcccactagac 426
                                                                                                gctgcagccattcctggtcatcgttgctgggtccacatgctggacaataatactggatct 180
                                                                                                                  gctgcagccattcctggtcatcgttgctgggtccacatgctggacaataatactggatct 366
                                                                                                                                                                                   ctggtttttattcttccctctctcatgttattaatccctcatatactgctagagaacttt 306
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/product= "Human transmembrane protein HP02000"
/note= "No stop codon given in the specification"
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100.0%; Pred. No. 7.8e-174;
                                                                                                                                                                                                                                                                                                         0; Mismatches
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WPI; 2001-367057/38
                          Sun W;
                                                                     12-JUL-1999;
                                                                                           12-JUL-2000; 2000WO-US18980.
                                            (META-) METABASIS THERAPEUTICS INC
                                                                                                                    18-JAN-2001.
                                                                                                                                              W0200104283-A2
                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                        Human; organic anion transporter; hOAT; liver; kidney;
                                                                                                                                                                                                                                                                                                          06-AUG-2001 (first entry)
                                                                                                                                                                                                                                                    membrane
                                                                                                                                                                                                                                                                                        hOAT5 DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein;
                                                                    99US-0143771.
                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                  /product= "hOAT5"
                                                                                                                                                                               /*tag=
                                                                                                                                                                                                                                             transport; organic anion; splice variant;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequences given in AAC85819-24 encode human organic anion transporter (hOAT) polypeptides. hOAT polypeptides are preferentially expressed in the liver and kidneys of humans. OAT's are membrane proteins that facilitate the transport of organic anions across the protein membrane. The mechanism of transport is thought to be a secondary or tertiary active transport involving exchange of another organic anion. hOAT2A and hOAT2B are thought to be splice variants as they are identical except at the C-terminal end. hOAT proteins and the DNA encoding them, may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate hOAT expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding human organic anion transporter polypeptides,
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Local Similarity 66.2%;
                                                                                                                                                  554
674 ggaggcatcataggtggccatgtctcagacaggtttgggcgaagatttattctcagatgg 733
                                       661
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                   ggaggcatcataggtggccatgtctcagac-----
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Pred. No. 3.6e-173;
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a Tool	948 gaaaaggcataaaaatgattgctacacaaaagtgaccaaattttaagaagccttcatgag	O V
181	aaaaaatctcaa	ф
947	933aaaaaaaatctcaag	Qy
17	1694 atcatttatggaatcttccccatcattggtggccttattgtcttcctcctaccagaaacc	ДĎ
932	933	Qy
16	1634 ggagcagcactggctcccctcttgatgaccttaacggtattttttaccacttttgccatgg	Дb
932		Qy
2 5	at	Db
152	. !	Qy
	cattg	Дb
3 2 2		Qy
, c	1454 tccattttggccaacacgtttgtgcccaaagaaatgcagaccctgcgtgtggctttggca	Дb
1 2	1	Qy
4	1394 acactaaatcatatgggccgtcgaataagccagatattgttcatgttcctggtgggcctt	Дb
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876	ttgtaagatccaccatgcaggaggagctggatgcagcacagaccaaaactactgtgtgt	2
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816	ttagaaaagttgcacgcacaaatggaataaagaatgctgaagaaaccctgaacatagag	Qy
1093	ggaatctgctcggtggttgataatcaccaataaactagatgagggcttaaaggca	Db
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7	914 ggtgcccttagtattggacagataatcctgggaggcttggcttatgtcttccgagactgg 9	Db
9	691 6	Qy
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U	794 tactgtgtactacgcttcttggcaggtttttcttccatgatcattatatcaaataattct 8	Db
9	691 6	Qy
9	734 tgtttgctccagcttgccattactgacacctgcgctgccttcgctcccaccttccctgtt 7	Db
9	6	Qy

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RESULT 5
AAK70136/c
ID AAK701
AC AAK701
XX AAK701
XX O6-NOV
XX O6-NOV
XX Human
XX Human;
KW Cytost
XX Cytost
XX Homo s
PN W02001
XX PO -AUG
XX PF 17-JAN
                  17-JAN-2001; 2001WO-US01354.
                                              09-AUG-2001.
                                                                                                                                  Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24948
                                                                  WO200157182-A2
                                                                                      Homo sapiens.
                                                                                                           cytostatic; gene
                                                                                                                        Human;
                                                                                                                                                              06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                            1667
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                                                                          2001US-0259678.
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                                              Ruben SM;
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Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -  $\,$ 

Disclosure; SEQ ID NO 24948; 3071pp + Sequence Listing; English

AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) ca amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic cativity, and can be used in gene therapy and vaccine production. (I) cativity, and can be used in gene therapy and vaccine production. (I) cativity, and can be used in gene therapy and vaccine production. (I) cativity, and can be used in gene therapy and vaccine production. (I) cativity of diseases associated with inappropriate (I) expression. For cativity of the production of the proteins or to that affect the activity of (I) by expressing inactive proteins or to catheticate the activity of (I) by expressing inactive proteins or to capplement the patients own production of (I). Additionally, (I) cathetic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, cathetic acids into a host cell and culturing the cell to express the cathetic cancids and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic antigen genomic cancers and cancer metastases of haematopoietic antigen genomic to sequences from the present invention. AAK54942 to AAK54950 and AAM82169 crantersent sequences used in the exemplification of the present invention. represent sequences used in the exemplification of the present invention.

Sequence 783 BP; 242 A; 119 C; 105 G; 317 T; 0 other;

Š 밁 δã B Š 밁 QΥ 밁 Š 밁 δÃ Qy 밁 20 QΥ 멍 20 밁 B Matches 773; Query Match Best Local : 1053 caccagaagggtttttttccctacaaccagcaagaacatatattagatacatgaatctca 1112 933 aaaaaaaatotoaaggaaaaggcataaaaatgattgctacacaaaagtgaccaaaatttta 992 1353 1293 ctggtgtatgaagcaccatgtgatgaattcataaagttgcaaaagtcaaaacaatactgt 536 1593 gtttacaatattataaagatattgttcaaattgaagggcaaaggccaggttcagcaattt 1652 476 296 416 CTCTTGAGCAATCTGATATTTTTGGGAAGTCCTTTAAAAAGTTACAAATTTATCAATAAA 477 CACCAGAAGGGTTTTTTTCCCTACAACCAGCAAGAACATATATTAGATACATGAATCTCA CATGATACTTTTGACATAATAAGCCATTGGAAAACGGAAAGATTAGATACTAAATAACAT 237 ACATGCAACCAGAAATCAAAATAAATCCAGAAATAGAGACCTATATAAATGCATTTAATA acatgcaaccagaaatcaaaataaatccagaaatagagacctatataaatgcatttaata CTGGTGTATGAAGCACCATGTGATGAATTCATAAAGTTGCAAAAGTCAAAAACAATACTGT Similarity Conservative 45.3%; Score 773; DB 22; 100.0%; Pred. No. 9.1e-167; 0; Mismatches 0; Length 783; Indels 0 Gaps 597 1412 1352 0,

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AAK70138/c

ID AAK70138 Standard; DNA; 782 BP.

XX AAK70138;

DT 06-NOV-2001 (first entry)

XX PD 06-NOV-2001 (first entry)

XX Human immune/haematopoietic antig

XX Human; immune; haematopoietic; im

XX PD 09-AUG-2001; 2001WC-US01354.

XX PD 09-AUG-2001; 2001WC-US01354.

XX PD 09-AUG-2001; 2000US-018665.

PR 04-FEB-2000; 2000US-0186664.

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PR 11-JUL-2000; 2000US-021688.

PR 11-JUL-2000; 2000US-022526.

PR 11-JUL-2000; 2000US-022526
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cytostatic; gene therapy; vaccine; metastasis; ds.
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CC anino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic CC archivity, and can be used in gene therapy and vaccine production. (I) CC proteins and polynucleotides may be used in the prevention, diagnosis and CC treatment of diseases associated with inappropriate (I) expression. For CC treatment of diseases associated with inappropriate (I) expression. For CC example, they may be used to treat disorders associated with decreased CC expression by rectifying mutations or deletions in a patient's genome CC that affect the activity of (I) by expressing inactive proteins or to CC that affect the activity of (I) by expressing inactive proteins or to CC supplement the patients own production of (I). Additionally, (I) CC supplement the patients own production of (I). Additionally, (I) CC orotein. (I) proteins and polynucleotides may be used to prevent, CC protein. (I) proteins and polynucleotides may be used to prevent. CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703 CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703 cancers and cancer metastases of haematopoietic antigen genomic to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK64942 to AAK94950 and AAM82169 cancers and cancers used in the exemplification of the present invention.
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Similarity 99.9%;
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16-MAR-2000
17-MAR-2000
18-APR-2000
19-MAY-2000
07-JUN-2000
28-JUN-2000
30-JUN-2000
07-JUL-2000
07-JUL-2000
11-JUL-2000
11-JUL-2000
                                                                                                                                                                                                                                                                                                                                              AAK70137 standard; DNA; 782 BP
                                                                                                                                                                                                                                                cytostatic; gene therapy; vaccine; metastasis; ds
                                                                                                                                                                                                                                                           Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
                                                                                                                                                                                                                                                                               Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24949.
                                                                                                                                                                                                                                                                                                       06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                            AAK70137;
                                                                                                                                                                                                                                                                                                                                                                                                                                         116 GTTTACAATATTATAAAGATATTGTTCAAATTGAAGGCCAAAAGGCCAGGTTCAGCAATTT
                                                                                                                                                                                       09-AUG-2001
                                                                                                                                                                                                                                Homo sapiens.
                                                                                                              24-FEB-2000;
02-MAR-2000;
                                                                                                                                               31-JAN-2000;
                                                                                                                                                                   17-JAN-2001; 2001WO-US01354.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATGATACTTTTGACATAATAAGCCATTGGAAAACGGAAAGATTAGATACTAAATAACAT 236
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  2000US-0184664
2000US-0186350
2000US-0189874
2000US-0190076
2000US-019123
2000US-0205467
2000US-021486
2000US-021486
2000US-021647
2000US-0216647
2000US-0216880
2000US-0217496
                                                                                                                                    2000US-0179065.
2000US-0180628.
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2000US-0218290 2000US-0220963

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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic proteins and gene therapy and vaccine production. (I) treatment of diseases associated with inappropriate (I) expression. For expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to polynucleotides may be used to freat disorders associated with decreased that affect the activity of (I) by expressing inactive proteins or to polynucleotides may be used to product on of (I). Additionally, (I) the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent,
                                                                                                                                                                                                                                                                                                                            17-NOV-2000
17-NOV-2000
17-NOV-2000
17-NOV-2000
17-NOV-2000
17-NOV-2000
17-NOV-2000
01-DEC-2000
01-DEC-2000
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05-DEC-2000
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06-DEC-2000
08-DEC-2000
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08-DEC-2000
08-DEC-2000
08-DEC-2000
                                                                                                                                                                Disclosure;
                                                                                                                                                                                                           Nucleic acids encoding
                                                                                                                                                                                                                                    WPI; 2001-483426/52.
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17-NOV-2000;
17-NOV-2000;
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08-NOV-2000;
08-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-NOV-2000;
                                                                                                                                                                                                     for
                                                                                                                                                                                                                                                                               HUMAN GENOME SCI INC
                                                                                                                                                                                          preventing, diagnosing and/or treating cancers and
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                                                                                                                                                                SEQ
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2000US-0251868.
2000US-0251869.
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2000US-0251990
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2000US-0249212.
2000US-0249213.
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2000US-0249209.
2000US-0249210.
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2000US-0246475

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2000US-0246477

2000US-0246478

2000US-0246523

2000US-0246525

2000US-0246526

2000US-0246526

2000US-0246526

2000US-0246528

2000US-0246528

2000US-0246528

2000US-0246538

2000US-0246538
                                                                                                                                                     ID NO 24949; 3071pp + Sequence Listing; English.
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01-SEP-2000 01-SEP-2000 05-SEP-2000 05-SEP-2000 06-SEP-2000 06-SEP-2000 08-SEP-2000 08-SEP-2000

2000US-022544 2000US-022688 2000US-0228924 2000US-0228924 2000US-0229345 2000US-0229345 2000US-0229503 2000US-0229503 2000US-0230438 2000US-0230438 2000US-0231242 2000US-0231242 2000US-0231244 2000US-0231244 2000US-0231241 2000US-0231241 2000US-0231241 2000US-0231241 2000US-0231241 2000US-0231241 2000US-023288 2000US-023288 2000US-023288 2000US-023289 2000US-023289 2000US-023289 2000US-023289 2000US-0232840 2000US-0233064 2000US-0233064

22-AUG-2000; 23-AUG-2000; 30-AUG-2000; 01-SEP-2000; 01-SEP-2000;

18-AUG-22-AUG-22-AUG-22-AUG-23-AUG-

> 2000US-0225267 2000US-0225268 2000US-0225270 2000US-0225277 2000US-0225477 2000US-022575758

02-OCT-2000 02-OCT-2000 02-OCT-2000 02-OCT-2000 13-OCT-2000 13-OCT-2000 20-OCT-2000 20-OCT-2000

2000US-0241960 2000US-0241221 2000US-0241785 2000US-0241786 2000US-0241787 2000US-0241808 2000US-0241808 2000US-0241809 2000US-0241826 2000US-0244817 21-SEP-2000 25-SEP-2000 25-SEP-2000 26-SEP-2000 27-SEP-2000 27-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000

2000US-0235836 2000US-0236327

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                           AAF55043;
                                                         AAF55043 standard; DNA; 1316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CACCAGAAGGGTTTTTTTCCCTACAACCAGCAAGAACATATATTAGATACATGAATCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGGTGTATGAAGCACCATGTGATGAATTCATAAAGTTGCAAAAGTCAAAACAATACTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTACTAGTAGATAAGATGATTCAGAAAACAAAAGAAATCACAGAATTAGGATGTGGCTGG
                                                                                                                                                                                                                                                    TTTAATTACTTTTCTTTGTAA-TTTTCTCTCTGTATATTTTAAACAAATAGCTGGTATA 117
                                                                                                                                                                                                                                                                                                                              ACATGCAACCAGAAATCAAAATAAATCCAGAAATAGAGACCTATATAAATGCATTTAATA
                                                                                                                                  tcaaactgtatgtacatttaataaaataactataaattaaaaaattatatttc 1705
                                                                                                                                                                                          GTTTACAATATTATAAAGATATTGTTCAAATTGAAGGGCAAAGGCCCAGGTTCAGCAATTT 57
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(first entry)
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Pred. No. 1.
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caccagaagggtttttttccctacaaccagcaagaacatatattagatacatgaatctca 1112 

645

caccagaagggttttttcccctacaaccagcaagaacatatattagatacatgaatctca

QΥ 망 QΥ Дb

Query Match Best Local Matches

Local

Similarity

43.3%; 98.7%;

Score 738.6; DB 22 Pred. No. 7.5e-159; Mismatches

DB 22;

Length 1316;

Indels

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Gaps

1:

755;

Conservative

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The present sequence encodes a calcium channel transport polypeptide. The polynucleotides, polypeptides, and antibodies are useful for preventing, treating, or ameliorating diseases associated with anomalies in calcium trafficking across the plasma membrane. They are used to diagnose, detect and treat or prevent diseases or conditions such as neural disorders (e.g. HIV-induced dementia), immune system disorders (e.g. rheumatoid arthritis), muscular disorders (e.g. muscle contractile dysfunction), reproductive disorders, gastrointestinal disorders, pulmonary disorders, cardiovascular disorders (e.g. arrhythmias), renal disorders, proliferative disorders, and/or cancerous diseases and conditions (e.g. lung carcinoma or breast cancer).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         proliferative disorder; cancer; lung carcinoma; breast cancer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Calcium channel transport polypeptide; calcium trafficking; neural disorder; HIV-induced dementia; immune system disorder; rheumatoid arthritis; muscular disorder; muscle contractile dysfunction; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; arrhythmia; renal disorder; cardiovascular disorder; arrhythmia; renal disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleotide sequence of a calcium channel transport polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-JUL-1999; 99US-0145958.
18-AUG-1999; 99US-0149446.
14-MAR-2000; 2000US-0189064.
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Sequence 1316 BP; 458 A; 227 C; 237 G; 394 T; 0 other;
                                                                                                                                                                                                                                                             Claim 1; Page 254; 259pp; English.
                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid useful for diagnosing, detecting, or treating or preventing diseases associated with anomalies in calcium trafficking
                                                                                                                                                                                                                                                                                                                                                                                               2001-138604/14.
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/product= "calcium channel transport polypeptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                              myeloid cell disorder; lymphoid cell disorder, asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiinflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
03-FEB-2000; 2000US-0496914.
27-APR-2000; 2000US-0560875.
                                                                                                            05-FEB-2001; 2001WO-US03800.
                                                                                                                                                                                                                                                                                                                                                                                                     antifungal; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         haematopoiesis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human secreted protein homologue-encoding cDNA, SEQ ID NO:752.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; cytokine; cell proliferation; cell differentiation; growth factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1653 tcaaactgtatgtacatttaataaaataactataaattaaaaaat 1697
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                                                                                                                                                                                                                                                                                                                                                                                                                        osteopathic; vasotropic; cardiant; virucide; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                             antiulcer;
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CC thrombolytic activities; receptor or ligand activities; or may be conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoletic disorders (e.g., myelold or lymphoid cell conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoletic disorders (e.g., myelold or lymphoid cell conditions, c.g., by protein or gene therapy. Such conditions include conditions, chronic inflammatory conditions (e.g., asthma or arthritis), correctly conditions include conditions conditions and abnormal conditions include inflammatory conditions, coronary heart disease, coronary heart disease, conditions in conditions and ulcers, while those with immunomodulatory activities may be used to promote wound immunomodulatory activities may be used in the treatment of viral, conditions with growth factor activity may be used in cell cultures to plypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells conditions and uncertain cells considered by illness, companied to augment or replace cells damaged by illness, and in drug screening techniques. The present sequence represents a cDNA encoding a covel human polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby glving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention management of the protein activities, including cytokine, cell proliferation or cell differentiation activities; stem cell growth factor activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      haematopoiesis regulatory activity; tissue growth activity; immunomodulatory activity; activin- or inhibin-related activities; chemotactic or chemokinetic activities; haemostatic, thrombotic or chemokinetic activities;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject, arthritis and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequences ABB10981-ABB12330 represent 1350 novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 677; 1963pp; English.
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Sequence 1353 BP; 349 A; 298 C; 315 G; 391 T; 0 other;

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tggcctttgaggagctcttgagtcaagttggaggccttggggagatttcagatgcttcatc
                                         ttgaacttatctccgtaaagccattgtgcctcctcttgggggtcacgtgttcacaatcaa
                                                          ttgaacttatctccgtaaagccattgtgcctcctcttgggggtcacgtgttcacaatcaa
                                                                                                                    attgatgogaggatcaatacaagottaatttgaattaataaaaggaaatattttctccct 127
                                                                                                                                                                             gaggaagctctttccactacggctgtattgcactggtgagtccggggcccatggatgaga
                                                                                                    attgatgcgaggatcaatacaagcttaatttgaattaataaaaggaaatattttctccct
                                                                                                                                                             gaggaagctctttccactacggctgtattgcactggtgagtccggggcccatggatgagaa 66
                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                          Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance, peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAI59215 standard; cDNA; 1375 BP.
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                                                                                                    21-JAN-2000;
25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                      Human polynucleotide SEQ ID NO 1418:
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 Tang YT,
Wang J,
                                                                                                                                                                                                                                                                                  leukaemia; ss.
                                                                                                                                                                              26-DEC-2000; 2000WO-US34263
                                                                                                                                                                                                                                 WO200153312-A1
                                      (HYSE-) HYSEQ INC.
                                                                            14-SEP-2000;
19-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               atcagtcactgaaatcagtggttcaattcctacttctgactggaatgctggtgggaggca
 Wang
  Liu C,
Wang Z,
                                                               2000US-0488725.
2000US-0552317.
2000US-0558042.
2000US-0620312.
2000US-0652450.
2000US-0662191.
2000US-0693036.
2000US-0727344.
     Wehrman T,
                Asundi V,
                 Chen R,
      Xu C,
        Ma Y,
Xue AJ,
         Qian XB,
Yang Y,
          Ren F, '
                        Wang
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, the encoded polypeptides (AAM38642-AAM42213) with nootropic process of the invention and cytostatic activity. The polynucleotides are useful immunosuppressant and cytostatic activity. The polypucleotide or no polypucleotide in gene therapy. A composition containing a polypeptide or polypucleotide of the invention may be used to treat diseases of the peripheral nervous of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as localised neuropathies and central nervous system diseases, such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, activity/nhibbin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and assays for receptor activity, arthritis and inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 1418; 10078pp; English.
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Note: The sequence data for this patent did not form part of the printed
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Pred. No. 2.2e-81;
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RESULT 11
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The present sequence is transporter and ion channel-10 (TRICH-10) cDNA. TRICH is used as vaccine. TRICH is useful for treating a disease or condition associated with decreased expression of functional TRICH, such as transport disorder including amyotrophic lateral sclerosis, cystic fibrosis, Becker's muscular dystrophy, Charcot-Marie Tooth neurological disorders including Alzheimer's disease, Duchenne muscular dystrophy, angina and hypertension, neurological disorders including Alzheimer's disease, amnesia, bipolar disorder, dementia, depression, epilepsy, ischaemic cerebrovascular
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Hillman JL, Azı...
YT, Khan FA;
                                                                                                                                               Claim 5; Page 147; 160pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                   14-JAN-2000;
21-JAN-2000;
28-JAN-2000;
02-FEB-2000;
                                                                                                                                                                                                 Novel human transporter and ion channel proteins useful for treating
                                                                                                                                                                                                                                                  P-PSDB; AAE04897
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene therapy; amyotrophic lateral sclerosis; amnesia; muscular dystrophy; hypertension; angina; neurological disorder; asthma; bipolar disorder; dementia; depression; Alzheimer's disease; apilepsy; vaccine; arrhythmia; huntington's disease; lachaemic cerebrovascular disease; AIDS; anxiety; stroke; demyelinating disease; mental disorder; cerebral neoplasm; allergy; muscle disorder; cardiomyopathy; cataract; myocarditis; Grave's disease; rheumatoid arthritis; Sjogren's syndrome; systemic lupus erythematosus; sickle cell anaemia; Wilson's disease; infertility; Cushing's disease; sickle cell anaemia; wilson's disease; infertility; cushing's disease; mallabsorption syndrome; hypercholesterolaemia; cancer; ss.
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2000US-0178572.
2000US-0179758.
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RESULT 12 AAC61892

AAC61892 standard; cDNA;

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725 ggcatcctaggcggtcatttatcagacaggt 755
                     664 ggcatcataggtggccatgtctcagacaggt 694
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Pred. No. 2.5e-81;
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cu useful in assays to determine their biological activities. The proteins of the proteins are also be used as biomarkers to identify tissues or cell types which cc express the proteins. The polynucleotide molecules can be used as comparable or chromosomes and to elicit immune responses. CC The proteins and antibodies are useful in diagnosis and treatment of comparable of the comparable 
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20-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel secreted human proteins useful for stimulating blood cell generation in patients receiving cancer chemotherapy, treating t marrow transplantation patients and for healing fractured bones
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAC61879-93 encode secreted human proteins. The secreted proteins are
                                                                                                                                                                                                                                                                                                                                             Sequence 2027 BP; 530 A; 501 C; 459 G; 537 T; 0 other;
                                                                                  124 cootttgaacttatotoogtaaagccattgtgcctcotcttgggggtcacgtgttcacaa 183
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                                                                                                                                                                                                                                                                                                                                            AAC85823;
                                                                                                                                                                                                                                                                                                   hOAT4 DNA
                                                                                                                                                                                                                                                                 membrane protein; transport; organic anion; splice variant; ds.
                                                                                                                                                                                                                                                                          Human; organic anion transporter; hOAT; liver; kidney;
                                                                                                                                                                                                                CDS
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                                                                                                                          12-JUL-2000; 2000WO-US18980.
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                                                                                                      12-JUL-1999;
                                                                                 (META-) METABASIS THERAPEUTICS INC.
                                         WPI; 2001-367057/38.
                                                              Sun W;
useful in gene therapy procedures
        Nucleic acids encoding human organic anion transporter polypeptides,
                            P-PSDB; AAB47275.
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                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                            9908-0143771.
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                                   AA161001;
                                                AAI61001 standard; cDNA; 1132 BP.
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                                                                                                                              661 ggaggcatcataggtggccatgtctcagacaggt 694
                                                                                                                                                     653 tgtgactctcaatcactgacttcagtggctaaatttgtattcatggctggaatgatgttg 712
                                                                                           14
                                                                                                                                                                      601 tgtgattatcagtcactgaaatcagtggttcaattcctacttctgactggaatgctggtg 660
                                                                                                                                                                                                         593 tgggtgtatgacagaatctccttctcatccaccatcggtgacctgaagtgggatctggta 652
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                                                                                                                                                                                                                                                                             484 cacctgaatgggactatccacagcacaagtgaggcagacacagaaccctgtgtggatggc 543
                                                                                                                                                                                                                                                                                                                  473 gactcaaacatgaggccagagaagtgtcgtcgctttgttcatcctcagtggcagctcctt 532
                                                                                                                                                                                                                                                                                                                                  424 gactcaaatctgaggccagagaagtgtcgtcgtctgtccatccccagtggcagcttctt 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequences given in AAC85819-24 encode human organic anion expressed in the liver and kidneys of humans. OAT's are preferentially proteins that facilitate the transport of organic anions or tertiary acclive transport involving exchange of another account is thought to be a secondary identical except at the C-terminal end. Hoar party active transport involving exchange of another organic anion. encoding them, may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate hoar expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184 tcaatggcctttgaggagctcttgagtcaagttggaggccttgggagatttcagatgctt 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1977 BP; 502 A; 491 C; 450 G; 534 T; 0 other;
                                                                                                                                                                                                                                                              cacctgaatgggaccttccccaacacaagtgacgcagacatggagccctgtgtggatggc 592
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                                                                                                                                                                                                                                                                                                                                                                       totgacaatgacactggggccctcagccaagatgcactcttgagaatctccatcccactg 472
                                                                                                                                                                                                                                                                                                                                                                                                                           ttcactgcattcatacctggccatcgctgctgggtccacatcctggacaatgacactgtc 412
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(first entry)
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ed. No. 1.5e-76;
Mismatches 150;
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                                                                                                                                                                                                                       the encoded polypeptides (AAM38642-AAM4223) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful gene therapy. A composition containing a polypeptide or polynucleotide system, such as peripheral nervous injuries, peripheral nervous alzheimer's, Parkinson's disease, Huntington's diseases, such as tetral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer disgnosis and thrapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S. discreases
                                                    379 ggaatcotcagtgaagatgccotcttgagaatctctatcccactagactcaaatctgagg 438
                                                                                                                                                                  Sequence 1132 BP; 274 A; 265 C; 285 G; 305 T; 3 other;
                                                                                                                                                                                             C.N.S disorders.
Note: The sequence data for this patent did not form part of the printed
                                     27 ggggccctcagccaagatgcactcttgagaatctccatcccactggactcaaacatgagg 86
                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                            The invention relates to human nucleic acids (AA157798-AA161369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic,
                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 4990; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tang YT,
Wang J,
Zhao QA,
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19-JUL-2000; 2000US-0520312
03-AUG-2000; 2000US-0653450
14-SEP-2000; 2000US-0663191
19-OCT-2000; 2000US-0693036
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                                                                                                                       264;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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                                                                                                                          h 13.7%;
Similarity 83.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001-442253/47.
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Wang z,
                                                                                                                 Conservative
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                                                                                                               ,0
                                                                                                                    Score 232.8; DB 2
Pred. No. 1.7e-43;
                                                                                                         Mismatches
                                                                                                                       _ DB_22; Length 1132;
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f. Yang Y,
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Qγ D,

499 atccacagcacaagtgaggcagacacagaaccctgtgtggatggctgggtatatgatcaa 558

87 ccagagaagtgtcgtcgctttgttcatcctcagtggcagctccttcacctgaatgggacc 146

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RESULT 15
AAD12566
ID AAD1256
XX AAD1251
XX AAD1251
XX AAD1251
XX Human;
KW Human;
KW Human;
KW Huntin,
KW Human;
FT CDS
FT CD
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The present sequence is human protein with hydrophobic domain encoding CDNA clone HP03613. The polynucleotide and polypeptide of the invention may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. The polynucleotides may be used to produce the polypeptide, by inserting the nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-JAN-2000; 2000JP-0000585.
06-JAN-2000; 2000JP-0000588.
11-JAN-2000; 2000JP-0002299.
03-FEB-2000; 2000JP-0026862.
03-MAR-2000; 2000JP-0058367.
                                                                                                                                                                                                         Claim 4; Page 252-257; 563pp; English.
                                                                                                                                                                                                                                                                   Human proteins with hydrophobic domains and the nucleic acids encoding them, useful for preventing diagnosing and treating e.g. cancer, Alzheimer's and inflammation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               contraceptive; antiinfertility; antiinflammatory; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= "Human protein having hydrophobic domain"
/note= "CDS is specifically is claimed in claim 3"
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                        635 tcctacttctgactggaatgctggtgggaggcatcataggttggccatgtctcagacaggt 694
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Search completed: July 1, 2002, 15:46:11 Job time: 6280 sec

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                                                                        organic anion transporter genes and proteins patent: WO 0104283-A 6 18-JAN-2001; Metabasis Therapeutics Inc. (US)
                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
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Direct Submission plinect Submission (10-MAR-2001) Whitehead Institute/MIT Center for Genome Submitted (10-MAR-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                             Zembek, L., Zimmer, A. and Zody, M.
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All repeats were identified using RepeatMasker:
smit, A.F.A. & Green, P. (1996-1997)
thttp://ftp.genome.washington.edu/RM/RepeatMasker.html
http://ftp.genome.Center
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Center clone name: 3110_P_
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/db_xref="taxon:9606"
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26437 AATGCATTTAATACATGATACTTTTGACATAATAAGCCATTGGAAAACGGGAAAGATTAGA 26378
                                                                                 26497 ADAACAATACTGTACATGCAACCAGAAATCAAAATAAATCCAGAAATAGAGACCTATATA 26438
                                                                                                                         26557 AGGATGTGGCTGGCTGTATGAAGCACCATGTGATGAATTCATAAAGTTGCAAAAGTC 26498
                                                   Matches
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                                                                                                                                                                 26617 ATTTATCAATAAATTACTAGTAGATAAGATGATTCAGAAACAAAAGAAAATCACAGAATT 26558
                                                                                                                                                                                                        1340 aaaacaatactgtacatgcaaccagaaatcaaaataaatccagaaatagagacctatata 1399
                                                                                                                                                                                                                                                1220 atttatcaataaattactagtagataagatgattcagaaacaaaagaaaatcacagaatt 1279
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45.4%; Score 774.8; DB 2; Length 164809;
Local Similarity 99.1%; Pred. No. 1.5e-141;
es 779; Conservative 0; Mismatches 7; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26197 GGTTCAGCAATTTTCAAACTGTATGTACATTTAATAAAAATAAGTATAAAATTAAAAAATTA 26138
                                                                                                                                                                                                                                                    Match 45.4%; Score 774.8; DB 9; Length 169776; Local Similarity 99.1%; Pred. No. 1.4e-141; Les 779; Conservative 0; Mismatches 7; Indels 0; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26257 AATAGCTGGTATAGTTTACAATATTATAAAGATATTGTTCAAATTGAAGGGCAAAGGCCA 26198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (24 APR-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, URL:http://hgp.gsc.riken.go.jp/, 750-761:81-45-503-9111, Fax:81-45-503-9170)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                              /clone="CTD-3110P2"
48281 a 32818 c 33507 g 55170 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
/chromosome="11"
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82826 AGGATGTGGCTGGTGTATGAAGCACCATGTGATGAATTCATAAAGTTGCAAAAGTC 82885
                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82886 AAAACAATACTGTACATGCAACCAGAAATCAAAATAAATCCAGAAATAGAGACCTATATA 82945
                                                                                                                                                                                                                                                                                                                                                       SOURCE
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                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82946 AATGCATTTAATACATGATACTTTTGACATAATAAGCCATTGGAAAACGGAAAGATTAGA 83005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1280 aggatgtggctggctggtgtatgaagcaccatgtgatgaattcataaagttgcaaaagtc 1339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1340 aaaacaatactgtacatgcaaccagaaatcaaaataaatccagaaatagagacctatata 1399
                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83066 TCCATGGTGGAATTTTAATTACTTTTTCTTTTGTAATTTTTTCTCTCTGTATATTTTAAACA 83125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1400 aatgcatttaatacatgatacttttgacataataagccattggaaaacggaaagattaga 1459
         COMMENT
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                                                                                                                                                                                                                                                                                                                                   ORGANISM
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                                                                                                                                                                                                                             TITLE
                                                                                                                                                                                                                                                             AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1580 aatagotggtatagtttacaatattataaagatattgttcaaattgaagggcaaaggcca 1639
                                                                                                                                       TITLE
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APU02367

Homo sapiens chromosome 11 clone RP11-151E18 map 11q, WORKING DRAFT

SEQUENCE, 9 unordered pieces.
                                                                                                                                   Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P., Hattori, M., Ishii, K., Totoki, Y., Watanabe, H. and Sakaki, Y. Fujiyama, A., Yada, T. Totoki, Y., Watanabe, H. and Sakaki, Y. Fujiyama, A., Yada, T. Totoki, Y., Watanabe, H. and Sakaki, Y. Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                          AP002367.1 GI:8131631
                           Submitted (29-MAY-2000) Masahira Hattori, The Institute of Physical Submitted (29-MAY-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); and Chemical Research (Strasato, Sagamihara, Kanagawa 228-8555, Kitasato Univ., 1-15-19 kitasato, Sagamihara, Kanagawa 228-8555, Japan (E-mail:hattori@gsc.riken.go.jp, Japan (E-mail:hattori@gsc.riken.go.jp), Tel:81-42-778-9923, URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923, Fax:81-42-778-9924)
                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                 HTGS_PHASE1;
                                                                                                                                                                                                                                                                                                                                                         sapiens DNA, clone:RP11-151E18.
Center: RIKEN Genomic Sciences Center(GSC)
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       * NOTE: This is a 'working draft' sequence. It currently sequences is consists of 9 contigs. The true order of the pleces is not known and their order in this sequence record as arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence runs of N, but the exact sizes of the gaps are unknown.
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Center clone name: RP11-151E18
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Contact: hattori@gsc.riken.go.jp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123106 123105: gap of 100 bp 123106 140640; contig of 17535 bp in length 123106 140640; contig of 17535 bp in length 140641 140740: gap of 12114 bp in length 152855; contig of 12114 bp in length 152855 161965; contig of 100 bp 161966 162065; gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 be preserved
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123106
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73754
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39394 73653; gap of 100 bp
73654 73753; gap of 25544 bp in length
73754 99297; contig of 2568 bp in length
99298 99397; gap of 100 bp
99398 123005; contig of 23608 bp in length
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165511 166848: contig of 1338
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73653 contig of
99297 contig of
123005 contig of
140640 contig of
152854 contig of
161965 contig of
1668410 contig of
166848 contig of
                 99398. .123005
/note="assembly_fragment"
123106. .140640
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73754 99207
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/chromosome="11"
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393: gap of 100 bp
73653: contig of 34260 bp in length
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34260 bp in length
25544 bp in length
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35911 GGTTCAGCAATTTTCAAACTGTATGTACATTTAATAAAATAACTATAAATTAAAAAATTA 35852
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                                                                                                                                                                                                                                                   36030 TCCATGGTGGAATTTTAATTACTTTTTTTTTTGTAA-TTTTCTCTCTGTATATTTTTAAACA 35972
                                                                                                                                         1640 ggttcagcaattttcaaactgtatgtacatttaataaaataactataaattaaaaatta 1699
                                                                                                                                                                                                                                                                                                                   1580 aatagctggttatagtttacaatattataaagataftgttcaaattgaagggcaaaggcca 1639
                                                                                                                                                                                                                                                                                                                                                                                  36150 AATGCATTTAATACATGATACTTTTGACATAATAAGCCATTGGAAAAACGGAAAGATTAGA 36091
                                                                                                                                                                                                                                                                     1520 tocatggtggaattttaattactttttctttgtaatttttctctctgtatattttaaaca 1579
                                                                                                                                                                                                                                                                                                                                   36210 AAAACAATACTGTACATGCAACCAGAAATCAAAATAAATCCAGAAATAGAGACCTATATA 36151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36270 AGGATGTGGCTGGCTGTATGAAGCACCATGTGATGAATTCATAAAGTTGCAAAAGTC 36211
                                                                                                                                                                                                                                                                                                                                                                                                  1400 aatgcatttaatacatgatacttttgacataataagccattggaaaacggaaagattaga 1459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36330 ATTTATCAATAAATTACTAGTAGATAAGATGATTCAGAAACAAAAGAAAATCACAGAATT 36271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1340 aaaacaatactgtacatgcaaccagaaatcaaaataaatccagaaatagagacctatata 1399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36390 GGGGACATGTAATCTCTTGAGCAATCTGATATTTTTGGGAAGTCCTTTAAAAAGTTACAA 36331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1280 aggatgtggctggctggtgtatgaagcaccatgtgatgaattcataaagttgcaaaagtc 1339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36450 TACATGAATCTCAATTATAATTATGGCATTAATTTGCATTTTATTTCAAAAATTAACTTGT 36391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36510 CAGGAAAAGAACACACAGAAGGGTTTTTTTCCCCTACAACCAGCAAGAACATATATTAGA 36451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1160 ggggacatgtaatctcttgagcaatctgatatttttgggaagtcctttaaaaagttacaa 1219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36630 TTGTTTTTCCAGAAAAAAAATCTCAAGGAAAAGGCATAAAAATGATTGCTACACAAAAG 36571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1100 tacatgaatctcaattataattatggcattaatttgcattttatttcaaaattaacttgt 1159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1040 caggaaaagaacacaccagaagggtttttttccctacaaccagcaagaacatatattaga 1099
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165511, .166848
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32391 c 31923 g 46064 t 801 others
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152955. .161965
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162066. .165410
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140741. .152854
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AC073256/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center project name; H_NH0204K20

Sequencing vector: M13; 100%
Sequencing vector: M13; 100%
Chemistry: Dye-primer ET; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 15744 bases at least 040
Consensus quality: 15744 bases at least 040
Consensus quality: 15094 bases at least 040
Insert size: 161080; agarose-fp
Onality roversace. 4 62 in 200 bases

Onality roversace. 4 62 in 200 bases

Onality roversace. 4 62 in 200 bases
                                                                                                                                                                                                                                                                                                                                                                                                * NOTE: This is a 'working draft' sequence. It currently * consists of 20 contigs. The true order of the pieces * is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouality coverage: 4.62 in 020 bases; agarose-fp Quality coverage: 4.50 in 020 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                     runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                         be preserved.
                                                                                                                                                                                                                                                                                                                                       as soon as it is available and the accession number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (12-JUN 2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, On Jun 16, 2000 this sequence version replaced gi:8468975.
                                                       19899
19999
24951
25051
30350
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11646
15817
15917
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Waterston, R.H. 170682)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence of Homo sapiens clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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2301
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19916: gap of unknown length 1998: contig of 3982 bp in len 24950: contig of 4952 bp in len 25050: gap of unknown length 30349: contig of 5299 bp in len 30349: contig of 5299 bp in len 36461: contig of 6012 bp in len 36561: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----- Project
                                                                                                                                                                            2200: contig of 2200 bp in length 2300: gap of unknown length 3481: contig of 1181 bp in length 4832: contig of 1251 bp in length 4932: gap of unknown length 6630: contig of 1698 bp in length 6730: gap of unknown length 11545: contig of 4815 bp in length 11645: contig of 4815 bp in length
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Matches Query Match

Local Sim

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                                                                             /note="assembly_name:Contig27"
ture 144600. .170682
ture /note="assembly_name:Contig28"
/note="assembly_name:Contig28"
51522 a 33360 c 33713 g 50161 t 1
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/note="assembly_name:Contig10"
3582. .4832
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
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94996: contig of 12254 bp in length
95096: gap of unknown length
108127: contig of 13031 bp in length
108227: gap of unknown length
127050: contig of 18833 bp in length
127150: gap of unknown length
144499: contig of 17349 bp in length
144599: gap of unknown length
144599: gap of unknown length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="assembly_name:Contig14" 15917. .19898
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11646. .15816
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="assembly_name:Contig15"
19999. .24950
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36562. .43193
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      44.6%;
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3: gap of unknown length
3: contig of 9137 bp in length
5: gap of unknown length
6: contig of 9782 bp in length
7: gap of unknown length
7: contig of 10061 bp in length
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      Score 761.2; DB 2;
pred. No. 6.5e-139;
                                                                                           1926 others
                             Length 170682;
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Db 134491 TTGTTTTTCCAGAAAAAAATCTCAAGGAAAAGGCATAAAAATGATTGCTACACAAAAG 134432
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                                                                                                                                                                                                                                                                                                                                                                                                              Matches 777; Conservative
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                                                                                                                                                                                                                                               Db 133712 TATTTC 133707
REFERENCE
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                                                              KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1160 ggggacatgtaatotottgagcaatotgatatttttgggaagtootttaaaaagttacaa 1219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
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                                                                                   LLDZ/3 DP DNA linear HTG 30-MAY-20 Homo sapiens chromosome 11 clone XXpac-662A14 map 11q13, WORKING DRAFT SEQUENCE, 29 unordered pieces. APO00596
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 116273)
                                                                          AP000596.2 GI:8118802
 Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
                                                  HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens DNA, clone:XXpac-662A14.
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98013 97912 contig of 1732 bp in length
98013 99744 contig of 1732 bp in length
101254 102868 contig of 1309 bp in length
102969 104921 contig of 1309 bp in length
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Published Only in DataBase (1999) In press
2 (bases 1 to 116,273)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality coverage: 4.03x in Q20 bases; sum-of-contigs
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44799
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Center clone name: xxpac-662Al4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://hgp.gsc.riken.go.jp/Contact: hattori@gsc.riken.go.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: RIKEN Genomic Sciences Center(GSC)
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113765: a-
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* This record will be updated with the finished sequence
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73839; gap of 100 bp
73940
77367
77466; gap of 100 bp
77467
80065; contig of 3427 bp in length
80066
80165; gap of 100 bp
80166
83825; contig of 2599 bp in length
83826 sgap of 100 bp
83926
83777; contig of 3660 bp in length
83926
83777; config of 2852 bp in length
83926
867778
868777; config of 2852 bp in length
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110942 112367; contig of 1426 bp in length
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99745 99844:
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44799 49514; contig of 4716 bp in length
49515 49614; gap of 100 bp
49615 55534; contig of 5920 bp in length
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55635 60136: con
/note="assembly_fragment"
44799. .49514
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                                                                                                  /note="assembly_fragment"
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/db_xref="taxon:9606"
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/map="11q13"
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114974: contig of 1209
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10841: contig of 2212 bp in length
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101153: con
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44698: contig of 6460
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contig of 1185 bp in length
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1280 aggatgtggctggctggtgtatgaagcaccatgtgatgaattcataaagttgcaaaagtc 1339
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49615. .55534
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55635. .60136
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95169...96734
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86878 .89783
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83926. .86777
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80166. .83825
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92852. 95068
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89884. .92751
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99845. .101153
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73940. .77366
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96840. .97912
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102969. .104921
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105022. .106500
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98.7%;
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Query Match 34.5%; Score 588; DB 9; Best Local Similarity 100.0%; Pred. No. 3.8e-10 Matches 588; Conservative 0; Mismatches 0
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1 (bases 1 to 160945)
1 (bases 1 to 160945)
1 Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y., Homo saplens genomic DNA published only in Database (2001) In press
2 (bases 1 to 160945)
2 (bases 1 to 160945)
3 Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens genomic DNA, chromosome 11q, clone:RP11-614K12
                                                                                                                                                                                                                                                                                                                 Submitted (16-MAR 2001) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 17-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Tel:81-45-503-9111, Fax:81-45-503-9170)
On Aug 27, 2001 this sequence version replaced gi:13383333.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complete sequence.
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                                                                                                                                                              /map="11q"
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                                                                                                                         and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan (E-mail:hattori@gsc.riken.go.jp,
                                                                                                                                                                               Direct Submission
Submitted (29-MAY-2000) Masahira Hattori, The Institute of Physical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCTCCCTTTGAACTTATCTCCGTAAAGCCATTGTGCCTCCTCTTGGGGGTCACGTGTTCA 143963
                                                                                                URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923.
Fax:81-42-778-9924)
                                                                                                                                                                                                                                                                 1 (bases 1 to 166848)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Wattanabe,H. and Sakaki,Y. Homo sapiens 166,848 genomic DNA of 11g
Published Only in DataBase (2000) In press
2 (bases 1 to 166848)
                                                                                                                                                                                                                              Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens DNA, clone:RP11-151E18.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AP002367.1 GI:8131631
Web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
                                                     Center: RIKEN Genomic Sciences Center(GSC)
                                             Center code: RIKEN
                                                                                  Genome Center
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39394
39653 contig of 34260 bp in length
39394
39653 contig of 25544 bp in length
99398
123005 contig of 25608 bp in length
140741
152854 contig of 12114 bp in length
152955
161965 contig of 9011 bp in length
162066
165410 contig of 9011 bp in length
165511
166848 contig of 3345 bp in length
165511
166848 contig of 3345 bp in length
165511
166848 contig of 3345 bp in length
165512
166848 contig of 1338 bp in length
165513 is a 'working draft' sequence. It currently
15 consists of 9 contigs. The true order of the pieces
15 not known and their order in this sequence record is
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39294 39393: gap of 100 bp
39394 73653: contig of 34260 bp in length
73654 73753: gap of 100 bp
73754 99297: contig of 25544 bp in length
99298 99397: gap of 100 bp
123005: contig of 23608 bp in length
123006 123105: gap of 100 bp
123106 140640: contig of 17535 bp in length
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165411 165510: gap of 100 bp
165511 166848: contig of 1338 bp in length
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Center project name: HumDraft11
Center clone name: RP11-151E18
                                          140741.
                                                                                                         /note="assembly_fragment"
123106. .140640
                                   /note="assembly_fragment"
140741. .152854
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39394. .73653
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99398. .123005
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Best Local Similarity 100.0%;
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55669 a 32391 c 31923 g 46064 t
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Homo sapiens 116,273 genomic DNA of 11913 published Only in DataBase (1999) In press 2 (bases 1 to 116273)
                                                                                                                                                                                                                                                       Homo sapiens chromosome 11 clone XXpac-662A14 map 11q13, WORKING DRAFT SEQUENCE, 29 unordered pieces
                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 116273)
                                                                                                                                                                                                                   AP000596.2 GI:8118802
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                                                                                                                                                                          sapiens DNA, clone:XXpac-662A14.
                                                                                                                                                                                                   HTGS_PHASE1;
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/note="assembly_fragment clone_end:T7 vector_side:left"
162066. .165410
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100.0%; Pred. No. 3.8e-105;
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\* arbitrary. Gaps between the contigs are represented as \* runs of N, but the exact sizes of the gaps are unknown. \* This record will be updated with the finished sequence \* as soon as it is available and the accession number will

be preserved.

sequence updated (26-May-2000).

\* NOTE: This is a 'working draft' sequence. It currently

\* consists of 29 contigs. The true order of the pieces

\* is not known and their order in this sequence record is

108630

110942

10660 105022

length length

length

length

length

length

115075

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URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923, pax:81-42-778-9924)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan (E-mail:hattori@ysc.riken.go.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (12-OCT-1999) Masahira Hattori, The Institute of Physical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       On May 31, 2000 this sequence version replaced gi:6997486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: This is a 'working draft' sequence. It currently consists of 29 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center clone name: XXpac-662A14

Center clone name: XXpac-662A14

Sequencing vector: PCR products; 100% of reads chemistry: Dye-terminator ET-amersham; 100% of reads chemistry: Dye-terminator ET-amersham; 290329

Assembly program: Phrap; version 0.990329

Assembly program: Phrap; version 1.684 Q40

Consensus quality: 103806 bases at least Q30

Consensus quality: 111869 bases at least Q30

Consensus quality: 111869 bases at least Q20

Insert size: 113473; sum-of-contigs

Quality coverage: 4.03x in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: hattori@gsc.riken.go.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center code: RIKEN
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* 77367 77466: gap of 100 bp

* 77367 77466: gap of 100 bp

* 77467 80065: contig of 3427 bp in length

* 77467 80065: contig of 2599 bp in length

80066 80165: gap of 100 bp

80166 83825: contig of 3660 bp in length

83826 83925: gap of 100 bp

83926 86771: contig of 3682 bp in length

86678 86877; gap of 100 bp

86678 89783: contig of 3682 bp in length
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92852 95068; contig of 2217 bp in length
95069 95168; gap of 100 bp
95169 96739; contig of 1571 bp in length
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113865: contig of 1198 bp in length
13765: gap of 100 bp
114974: contig of 1209 bp in length
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5600: gap of 1479 bp in length
108529: confir ~ 100 bp
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2968: gap of 100 bp
104921: contig of 1953 bp in length
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89783: contig of 2906 bp in length
183: gap of 100 bp
92751: contig of 2868 bp in length
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39: contig of 2352 bp in length
gap of 100 bp
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                                                             Db 111996 GGATCTGGTAATGAAACTGGAATCCTCAGTGAAGATGCCCTCTTGAGAATCTCTATCCCA 112055
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421 ctagactcaaatctgaggccagagaagtgtcgtcgctttgtccatccccagtggcagctt 480
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                                                                                     361 ggatctggtaatgaaactggaatcctcagtgaagatgccctcttgagaatctctatccca 420
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106601, .108529
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98013. .99744
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95169. .96739
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96840. .97912
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80166. 83825
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60237. .65623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 586.4; DB 2;
Pred. No. 8.2e-105;
0; Mismatches 1;
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FEATURES

114975 115074: gap of 115075 116273: cont

Location/Qualifiers

112368 112467; gap of 112468 112468 112467

113666 113765:

108530 108629: gap of 108630 110841: cont

106501 106600:

104922 105021: gap of

02869 102968:

71388 71487:

73839

65624 65723: 0103 70202:

source

misc\_feature misc\_feature misc\_teature misc\_feature misc\_feature

/note="assembly\_fragment" /note="assembly\_fragment"

.60136

'note="assembly\_fragment"

/map="11q13" /chromosome="11" /organism="Homo sapiens" /db\_xref="taxon:9606"

XXpac-662A14"

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Db 112116 CTTCACCTGAATGGGACTATCCACAGCACAAGTGAGGCAGACACAGAACCCTGTGTGGAT 112175
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Mammaalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

CDNA Sequencing by: Sequencing Group at the Scanford Human Genome

DNA Sequencing by: Sequencing Group at the Stanford, CA 943

Center, Stanford University School of Medicine, Stanford, CA 943

Center, Stanford, edu

Web site:

Contact: (Dickson, Mark) mcdepaxil.stanford.edu

Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH
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/db_xref="taxon:9606"
/clone="MGC:23972 IMAGE:4714598"
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/protein_id="aah22379.1"
/db_xref="q1:18490378
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pghrGwrhILDNDTVSDNDTGALSQDALLRISIPLDSNNRFEKCRFVHAGMNVGG
GTFRNTSDADMEPCVDGWVYDRISFSSTIVTEWDLVCDSQSLTSVAKFVFMAGMNVGG
GTFRNTSDADMEPCVDGWVYDRISFSSTIVTEWDLVCDSQSLTSVAKFVFMAGWNVGTIL
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/clone_lib="NIH_MGC_76"
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                                                                                                                                     TITLE
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                                                                                                                                                                                                                                                                                                                   1986 bp
Sequence 37 from Patent WOO146258.
AX179749
                                                                                                             Baughn, M.R., Burford, N., Au-Young, J., Lu, D.A., Yang, J., Lal, P., Hillman, J.L., Azimzai, Y., Yue, H., Nguyen, D.B., Y Gandhi, A.R., Tang, Y.T. and Khan, F.A.
Transporters and ion channels
Patent: WO 0146258-A 37 28-UUN-2001;
Transporters
                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1986)
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                                                                                                      Incyte Genomics, Inc.
              /organism="Homo sapiens"
/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="Incyte ID No: 3358383CB1"
/note="Incyte ID No: 3528 t
496 c 457 g 528 t
                                                                                     ocation/Qualifiers
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O. Mismatches 150;
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725 GCCATCCTAGGCGGTCATTTATCAGACAGGT 755
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                Takanaga,H., Ohtsuki,S. and Terasaki,T.
Direct Submission
Submitted (26-MAY-2001) Hitomi Takanaga, Tohoku University,
Graduate School of Pharmaceutical Sciences; Aramaki, Aoba, Sendai,
Aoba-ku, Miyagi 980-8578, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Takanaga,H., Ohtsuki,S., Hosoya,K. and Terasaki,T. Isolation of novel clone of amphiphilic solute facilitator family from human fetal liver
                                                                                                                                                                                                                    Eukaryola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                      648 tggaatgctggtgggaggcatcataggtggccatgtctcagacaggt 694
                                                                                        588 gtgggacctggtatgtgattatcagtcactgaaatcagtggttcaattcctacttctgac 647
                                                                    503 GTGGGATCTGGTATGTGACTCTCAATCACTGACTTCAGTGGCTAAATTTGTATTCATGGC
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Fax:81-22-217-6886)
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/DE xref="GI::8148873:"
/db_xref="GI::8148873:"
/tans.lation="marfollchagdlwrefoilotvelsifavatylhemlenetafi
/tans.lation="marfollchagdlwrefoilotvelsgilsvakevemagmvgg
gffentschamsecvogmvydrisfsstivtewdlvclosgslysvakevemagmwvgg
MLIAEMLSDREGREFVLRWCYLOVAIVGTCAALAPTFLIYCSLRFLSGIAAMSLITINTI
SWILLSBREGREFOLAWGTIGMVCPSGIAFMTLAGLAFAIRWHIIQLVVSVPYEVIFLTS
SWILLSARWLIINNKPEEGLKELRKAAHRSGWKNAROTLTEILKSTMKKELEAAOKK
ANCVAPWALKYNNRRASGWKLMFLAGLLAFITFVPDEMOTLREVLATLGQTLEGAVILL
TLAFAHGNEVIFTIIRARAMGINATFANIAGALAPLMMILSVYSPPLPWIIVGVEPFI
TCEPARTIC DGTMANTENTATANIAGALAPLMMILSVYSPPLPWIIVGVEPFI
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102. .1763
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(bases 1 to 1846)

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TITLE AUTHORS SOURCE KEYWORDS

AB062418.1 GI:18148872

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                                                                                                              TGGGTGTATGACAGAATCTCCTTCTCATCCACCATCGGTGACCTGAAGTGGGATCTGGTA
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                                                    TGTGACTCTCAATCACTGACTTCAGTGGCTAAATTTGTATTCATGGCTGGAATGATGTTG
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Location/Qualifiers
1. 1977
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 gaagetettteeaetaeggetgtattgeaetggtgagteegggeeeatggatgagaaatt 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71
aaatctgaggccagagaagtgtcgtcgctttgtccatccccagtggcagcttcttcacct 488
                                                                CAATGACCCTGGGACCCTCAGCCAGGATGCCCTCCTGAGAATCTCCATCCCATTCGACTC
                                                                                                                                                                         tgcagccattcctggtcatcgttgctgggtccacatgctggacaataatactggatctgg 368
                                                                                                                                                                                                                                                                                                            GGCCTTTCAGGACCTCCTAGATCAAGTTGGAGGCCTGGGGAGATTCCAGATCCTTCAGAT 83404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGGTCAGGATCAACACACACACTTAGTGTGATTTAAGGAAAGGAAATATTTTCT--CTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  taatgaaactggaatcctcagtgaagatgccctcttgagaatctctatcccactagactc 428
                                                                                                                                                 AGCATTCATACTTGATCATCGCTGCTGGGTTCATATACTGGACAATGACACTATCCCTGA 83284
                                                                                                                                                                                                                                 GGTTTTCCTTATAATGTTCAACGTCATAGTATACCATCAAACTCAGCTGGAGAACTTCGC
                                                                                                                                                                                                                                                      99cctttgaggagctcttgagtcaagttggaggccttgggagatttcagatgcttcatct 248
                                                                                                                                                                                                                                                                                                                                                                                              TGAACTTATCTGGATACAGTCATTTTGTCTCCTCTTGGGGATCACTTGTCCAGCCTCAAT 83464
                                                                                                                                                                                                                                                                                                                                                                                                                 and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattoriégsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 160945)

Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,

Hughama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

Homo sapiens genomic DNA

Published Only in Database (2001) In press

2 (bases 1 to 160945)

Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,

Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

Direct Submission 2001, Yang, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             On Aug 27, 2001 this sequence version replaced gi:13383333.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (16-MAR-2001) Masahira Hattori, The Institute of Physical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complete sequence. AP003420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens genomic DNA, chromosome 11q, clone:RP11-614K12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens DNA, clone:RP11-614K12
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31738 c 32047 g 50417
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 340.8; DB 9; Pred. No. 6e-57;
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
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Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K.,
McRenan, R., McKernan, K.,
McCarthy, M., McEwan, P., McKernan, K.,
McCarthy, M., McCarthy, M., McEwan, P., McKernan, K.,
McCannor, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H.,
O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K.,
Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R.,
Phunkhang, P., Pierre, N., Pollara, V., Roymond, C., Retta, R.,
Rhieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M.,
Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P.,
Strauss, C., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, M., Straushanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A.,
Milson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J.,
Rembek, I., Zimmer A., and Zody W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (10-MAR-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Jun 11, 2001 this sequence version replaced gi:13270647. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wilson, B., Wu, X., Wyman, D., Ye, W Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 157859 bases at least Q40 Consensus quality: 161528 bases at least Q30 Consensus quality: 162334 bases at least Q20 Insert size: 172000; agarose-fp
                                                                                                                                                                                                                                                                                                     Center project name: L12735
Center clone name: 3110_P_2
                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                         ----- Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                     Sequencing vector: Plasmid; n/a;
Insert size: 163409; sum-of-contigs
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                                                                                                                                                                                                                                                                            Summary Statistics
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                                                                                                                                                                                                                                        100% of reads
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This record will be updated with the finished sequence
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12556 15164: contig of 2609 bp in length
15165 15264: gap of 100 bp
15265 16648: contig of 1384 bp in length
16649 16748: gap of 100 bp
16749 29429: contig of 12681 bp in length
29430 29529: gap of 100 bp
29530 41226: contig of 11697 bp in length
41227 41326: gap of 100 bp
41327 57370: contig of 16044 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8419 10046: contig of 1628 bp in length 10047 10146: gap of 100 bp 10147 12455: contig of 2309 bp in length 12456 12556: contig of 2309 bp in length
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4881 4980: gap of 10
4981 6768: contin - 1
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6868: gap of 100 bp

6868: gap of 100 bp

8318: contig of 1450 bp in length

6868: gap of 100 bp
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'9: gap of 100 bp

3440: contin of 200 bp
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                                                                    Organic anion transporter genes and proteins patent: WO 0104283-A 6 18 JAN-2001; Metabasis Therapeutics Inc. (US)
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                                                                                submitted (16-MAR-2001) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Schences Center (GSC); 1-7-22 Suehitro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
On Aug 27, 2001 this sequence version replaced gi:13383333.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               508;
                                                                                                                                                                                                                        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 160945)

Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Homo sapiens genomic DNA
Published only in Database (2001) In press

2 (bases 1 to 160945)

Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens genomic DNA, chromosome
                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                   /db_xref="taxon:9606"
                                              /organism="Homo sapiens"
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JOURNAL REFERENCE
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                                                                                                                                                                                                                             and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923, Fax:81-42-778-9924)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyana,A., Yadda,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Homo sapiens 166,848 genomic DNA of 11q Published Only in DataBase (2000) In press 2 (Dases 1 to 166848)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yadda,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (29-MAY-2000) Masahira Hattori, The Institute of Physical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                       Web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
                                                                                                            Center code: RIKEN
                                                                                                                                                   Center: RIKEN Genomic Sciences Center(GSC)
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Project Information
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FEATURES
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39394 73653 contig of 34260 bp in length
73754 99297 contig of 23608 bp in length
99398 123005 contig of 23608 bp in length
140741 152854 contig of 17535 bp in length
140741 152854 contig of 17535 bp in length
152955 161965 contig of 12114 bp in length
162066 165410 contig of 9011 bp in length
165215 166848 contig of 3345 bp in length
165511 166848 contig of 3345 bp in length
165511 166848 contig of 1338 bp in length
165512 166848 contig of 1338 bp in length
16513 1 166848 contig of 1338 bp in length
16511 16513 1 166848 contig of 1338 bp in length
16511 166848 contig of 1338 bp in length
165210 the pincere

* This is a 'working draft' sequence. It currently

* tons of y contigs. The true order of the pincere

* This record will be updated with the finished sequence

* This record will be updated with the finished sequence

* This record will be updated with the finished sequence

* This record will available and the accession number will
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Assembly program: Phrap; version 0.990329
Consensus quality: 162010 bases at least Q30
Consensus quality: 164639 bases at least Q30
Consensus quality: 165330 bases at least Q20
Insert size: 166048; sum-of-contigs
Quality coverage: 6.27x in Q20 bases; sum-of-contigs
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123106 14064(
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39294 39393; gap of 100 bp
39394 73653; contig of 34260 bp in length
73654 73753; gap of 100 bp
73754 99297; contig of 25544 bp in length
73754 99297; contig of 25546 bp in length
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140641 152854; contig of 12114 bp in length
140741 152854; gap of 100 bp
152855 152954; gap of 9011 bp in length
152955 161965; gap of 100 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
      /note="assembly_fragment"
152955. .161965
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73754. .99297
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                                                                   140741. .152854
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140640: CT
1740
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contig of 17535 bp in length
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VERSION
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Local Similarity 100.0%; Pred. No. 1.5e-105;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens genomic DNA, chromosome 11q, clone:CTD-3110P2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complete sequences.
                                                                                     and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi ku, Yokohama, Kanagawa 230-0045, Japan
[E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens DNA, clone:CTD-3110P2
                                                                                                                                                                   Submitted (24-APR-2000) Masahira Hattori, The Institute of Physical
                                                                         On Apr 26,
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165511. 166848
/note="assembly_fragment"
1 32391 c 31923 g 46064 t 801 others
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162066. .165410
                                    , 2001 this sequence version replaced gi:10716820. Location/Qualifiers
1. .169776
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                  /organism="Homo sapiens"
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/chromosome="11"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 gtatatgatcaaagctacttcccttcgaccattgtgactaag 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 ctgaatgggactatccacagcacaagtgaggcagacacagaaccctgtgtggatggctgg 360
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              Sequencing vector: M13; 100%
Sequencing vector: plasmid; 0%
                                                                                                                                                                     MO 63108, τις
On Jun 16, ?
                                                           Center project name: H_NH0204K20
                                                                                  Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                               Direct Submission
Submitted (12-JUN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                    Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                                                                                              Waterston, R.H.
                                                                                                                                  ----- Genome Center
                                                                                                                                                                                                                                                                            Unpublished
                                                                                                                                                                                                                                                                               The sequence of Homo sapiens clone
                                                                                                                                                                                                                                                                                                       Waterston, R.H.
                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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100.0%; Pred. No. 1.5e-105;
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* NOTE: This is a 'working draft' sequence. It currently consists of 20 contigs. The true order of the places is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality coverage: 4.50 in Q20 bases; agarose-fp Quality coverage: 4.50 in Q20 bases; sum-of-contigs
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Insert size: 168782; sum-of-contigs
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11646
15817
/note="assembly_name:Contig12" 6731. .11545
                                                                                                                                                                                                               2301
                                                                            /note="assembly_name:Contig11"
                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="11"
                                                                                                                                              /note="assembly_name:Contig10
                                                                                                                                                                                                                   /note="assembly_name:Contig9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .17068
                                                                                                                                                                                                                                                                                                   /clone="RP11-204K20"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108227: gap of unknown length
127050: contig of 18823 bp in length
127150: gap of unknown length
144499: contig of 17349 bp in length
144599: gap of unknown length
170682: contig of 26083 bp in length
                                                                                                                                   .4832
                                                                     . 6630
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2300: gap of unknown length
3481: contig of 1181 bp in length
4832: gap of unknown length
4832: contig of 1251 bp in length
4932: gap of unknown length
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0: gap of unknown length
5: contig of 4815 bp in length
5: gap of unknown length
6: contig of 4171 bp in length
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contig of 12254 bp in length
gap of unknown length
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contry of 3982 bp in length
contry of unknown length
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Ig of 5299 bp in length

inknown length

inknown length
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lg of 4952 bp in length
of unknown length
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of 6632
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144600. .170682
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43294. .52430
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11646. .15816
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19999. .24950
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72574. .82642
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127151. .144499
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Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Homo sapiens 116,273 genomic DNA of 11q13
Published Only in DataBase (1999) In press
2 (bases 1 to 116273)
2 (bases 1 to 116273)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
Direct Submission
Submitted (12-0CT-1999) Massahira Hattori, The Institute of Physical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Yapan (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923, Fax:81-42-778-9924)
On May 31, 2000 this sequence version replaced gi:6997486.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       preserved
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29 contigs. The true order of the minor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center project Information
Center project name: Humbraftl1
Center clone name: Xypac-662A14
Center clone name: Xypac-652A14
Center clone name: Xypac-652A14

Sequencing vector: PCR products; 100% of reads
Sequencing vector: PCR products; 100% of reads
Chemistry: Dye-terminator ET-amersham; 100% of reads
Assembly program: phrap; version 0.990329
Consensus quality: 103806 bases at least Q40
Consensus quality: 113869 bases at least Q20
Consensus quality: 113869 bases at least Q20
Insert size: 113473; sum-of-contigs
Quality coverage: 4.03x in Q20 bases; sum-of-contigs
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1 (bases 1 to 116273)
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99845
101254
102969
105022
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Contact: hattori@gsc.riken.go.jp
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sapiens DNA, clone:XXpac-662A14.
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38239 44698: contig of 6460 bp in length
44699 44798: gap of 100 bp
44799 49514: contig of 4716 bp in length
49515 49614: gap of 100 bp
49515 49614: gap of 100 bp
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24 70102: contig of 4379 bp in 16

03 70202: gap of 100 bp

03 71387: contig of 1185 bp in 16

88 71487: gap of 100 bp

88 71487: gap of 2352 bp in 16
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55635. .60136
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101254. .102868
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77467. .80065
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Submitted (O1-FEB-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Cance
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Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1566)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH
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                                                                                    PGHRCWVHILDNDTVSDNDTGALSQDALLRISIPLDSNMRPEKCRRFVHPQWQLLHLN
GTFPNTSDADMEPCVDGWVYDRISFSSTIVTEWDLVCDSQSLTSVAKFVFMAGMMVGG
ILGGHLSDSSRVGNTQIPGHGNYIGNVPFWYCIYDPGRPGFCHSRLAYPPAGGVCTIL
                                                CDLSDLKLAARVCSVAHYQQ"
                                                                                                                                                                                                                                                    /product="Similar to ust3"
/protein_id="AAH22379.1"
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/tlssue_type="Liver"
/clone_lib="WIH_MGC_76"
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(Dickson, Mark) mcd@paxil.stanford.edu
M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
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                                                                                                                    Graduate School of Pharmaceutical Sciences; Aramaki, Aoba, Aoba-ku, Miyagi 980-8578, Japan (B-mail:takanaraamsi) ---
                                                                                                                                                                                                                                                              Takanaga, H., Ohtsuki, S., Hosoya, K. and Terasaki, T. isolation of novel clone of amphiphilic solute facilitator
                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens ust3 mRNA for hUST3, AB062418
                                                                                                  Fax:81-22-217-6886)
                                                                                                                                                                                              Takanaga, H., Ohtsuki, S. and Terasaki, T.
                                                                                                                                                                                                                             Unpublished
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                  from human fetal liver
                                                                                                                  (E-mail:takanaga@mail.pharm.tohoku.ac.jp,
                                                                                                                                                                                                              (bases 1 to 1846)
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/tissue_lib="fetal liver" 102. .1763
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Homo sapiens
Eukaryota; Metazoa;
Mammalia; Eutheria;
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TLAFAHGNEVIFTIRARAMGINATFANIAGALAPLMYILSVYSPPLPWIIYGVFPFI
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37 from Patent W00146258
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 Chordata;
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   Hominidae;
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                 Euteleostomi;
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                                         Sun, W.
                                                                                                                                                                Sequence 5 from Patent W00104283.
              Patent:
                            Organic
                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                      Homo sapiens
Metabasis Therapeutics
                                                                                                                                                     AX074149.1
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Baughn,M.R., Burford,N., Au-Young,J., Lu,D.A., Yang,J.,
Lal,P., Hillman,J.L., Azimzai,Y., Yue,H., Nguyen,D.B., )
Gandhi,A.R., Tang,Y.T. and Khan,F.A.
Transporters and ion channels
Patent: WO 0146528-A 37 28-JUN-2001;
Incyte Genomics, Inc. (US)
                                                         (bases 1 to 1977)
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           anion transporter genes and WO 0104283-A 5 18-JAN-2001;
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/db_xref="taxon:9606"
/note="Incyte ID No: 3358383CB1"
496 c 457 g 528 t
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1. .1986
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395; Conserv
    Direct Submission Submitted (10-DEC-1996) D.
                                                                           Molecular cloning and characterization proteins from rat kidney FEBS Lett. 425 (1), 79-86 (1998)
                                                                                                                                 1 (bases 1 to 2597) Schomig, E., Spitzenberger, F., Engelhardt, M., Martel, F., Ording, N.
                                    Gruendemann,D.
                                                                                                                          and Grundemann, D.
                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                     Rattus norvegicus
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                                                                                                                                                                                                                                             integral membrane transport protein; UST1r gene
                                                                                                                                                                                                                                                                                    protein (UST1r).
Y09945
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1. .1977
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/db_xref="taxon:9606"
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University of Heidelberg
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Local Similarity 74.4%;
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                                                                    TOTCAGTCACTGGATTCAATAGCTAAGTTTCTATTCTTGACTGGTATCTTAGTAGGAAAT
ATCCTATATGGCCCCTTAACAGACAGGT 594
                                                                                            tatcagtcactgaaatcagtggttcaattcctacttctgactggaatgctggtgggaggc 480
                                                                                                                                                   GTGTATGACCAAAGCACCTTTCTTTCCACCATTATTACCGAGTGGGACCTGGTGTGAA
                                                                                                                                                                       gtatatgatcaaagctacttcccttcgaccattgtgactaagtgggacctggtatgtgat 420
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87. 17.
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SALVHANELLFTIIRATALGVIGIAGSTGAALSPLFMILRTYSDSLPWIIYGVLSFLG
GLVVLLLPETKNQPLPDSIQDVENEGRASRQGKQNDTLIKVTQF"
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phhrcwvpildndtvsgndngnlsqddllrvsipldsdlrpekcrrevopqwdllhln
gtessytedptepcydgwyrdgstelstiftemdlyoesqsldakfeletigilygn
ilygpltdregrrlilicaslomvtetcaarapteliycslrelagisestytunsa
lliibwtrpkroalarglllcaslomvtetcaarapteliycslrelagisestylpt
rwlsesarwlimtnklokglkelikvahingmknstdyltieyvriimkeelbasgtk
sslwdlfriphlrkricllslyreyvwlsyigllinghlrinyfllochlgiitipa
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/protein_id="CAA71076.1"
/db_xref="GI:3004482"
/db_xref="SPTREMBL:070609"
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87. .1745
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Pred. No. 5.6e-76;
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Best Local
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tcaaatctgaggccagagaagtgtcgtcgctttgtccatccccagtggcagcttcttcac
                                                                                  GATAATAACAGTAGGATCCTGAGCCAAGATGACCTCCTAAGGATCTCCATCCCAATGGAC
                                                                                                          ggtaatgaaactggaatcctcagtgaagatgccctcttgagaatctctatcccactagac
                                                                                                                                                                                                                                   gctgcagccattcctggtcatcgttgctgggtccacatgctggacaataatactggatct 180
                                                                                                                                                                                                                                                                                               TTGATTTTTGTACTGATCTGCTTTATCCTGGTAGTTCCTCACACTGTTTTGGAGAACTTC
                                                                                                                                                                                                                                                                                                                                              ctggtttttattcttccctctctcatgttattaatccctcatatactgctagagaacttt 120
                                                                                                                                                                                                                                                                                                                                                                                                    ATGGCCTTTCAGGACCTTATAACTCAAATTGGCTGCCTGGGGAGGTTCCAGATCCTTCAC 180
                                                                                                                                                                                          ACTGCAGCCATTCCTAGTCATCGCTGTTGGGTCCCCATCCTCGACAATAACACTATGTCT
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422 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (28-NOV-2000) Seok Ho Cha, Kyorin University School Medicine, Department of Pharmacolgy and Toxicology; 6-20-2 Shinkawa, Mitaka, Tokyo 181-8611, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cha,S., Sekine,T., Ono,T., Hasegawa,M., Kanai,Y. and Endou,H. Molecular cloning and characterization of multispecific organic anion transporter 5 expressed in the kidney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (strain:Sprague-Dawley) cDNA to clone_lib:rat kidney cDNA library clone:rOAT5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (sites)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="organic anion transporter 5"
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/translation="MARQDLITQIGCIGREQILHLIFVLICFILVVPHTVLENFTAAI
PSHRCWVPILDNITMSDNNSRILSQDDLLRISIPMDSNLRPEKCRRYIQPQWDLLHLN
GTESTVTEPDFEVDGWVXDGSTELSTTVTQMDLVCGSCTLNSVAKFILTGISSSCIRRNSA
LLILEWTSPKRQAMVMALIFSAAGIGQVLLGVLAFGIRNWQHLQLAMSVPVFFLLIPT
RWLSBSARWLIITNKPQEGLKELKVAHINGIRNSRDVLTLEVVKTTMKDELEAAETK
PSPLVLFRTPMNRKRICLESFVRCVSLISTVGLLINGVLSNKVFLOLYGVVCTPA
NLLNWESMNYMGRETTQGILTSTVGLLINGVLSNKVFLOLYGVVCTPA
NLLNWESMNYMGRETTQGILTSTFLTQEMQIPRLVLASLGGAISSASIT
STAVLSNELVPTVIRATALGVIGIFGSAGAALSPLLMILMTYSASLPWIIYGVLPILS
SLVVLLLPETRNQPLPDSIQDVENKRKSSREVKKDAVAKVTPF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 il:nalgo@kyorin-u.ac.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="rat kidney cDNA library"
121. .1776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="rOAT5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ocation/Qualifiers
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73.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 293.6; DB 10; Pred. No. 4.1e-74;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi;
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TITLE
JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shiohata, N., Matsumoto, K., Hirano, M., Sano, S., Nomura, R., Voshikawa, Y., Matsumoto, K., Hirano, M., Sano, S., Chiba, E., Momiyama, H., Voshikawa, Y., Matsumara, Y., Moriya, S., Chiba, E., Momiyama, H., Onogawa, S., Kaeriyama, S., Satoh, N., Matsunawa, H., Takahashi, E., Rataoka, R., Kuya, N., Kuroda, A., Satoh, I., Kamata, K., Takami, S., Terashima, Y., Watanabe, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Ota, T., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Kawai-Hio, Y., Saito, K., Washikawa, T., Kimura, K., Yamashita, H., Wanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T.
                                                                                                                                                                                                                                                                                                                                                Isogai, T., Otsuki, T. and Sugiyama, T.

Direct Submission
Submitted (24-0CT-2001) Takao Isogai, Helix Research Institute,
Submitted (24-0CT-2001) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(B-mail:genomics@hri.co.jp, Tel:81-438-52-3951, Fax:81-438-52-3952)
NEDO human cDNA sequencing project supported by Mnistry of
Economy, Trade and Industry of Japan; CDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
Construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'- 6 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AKU57654.1 GI:16553416
AKU57654.1 GI:16553416
oligo capping; fis (full insert sequence).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                             Evaluation; clone selection for full insert sequencing: RAB and
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                                                                                                                /tissue_type="trachea"
/clone_lib="TRACH2"
                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                 /clone="TRACH2000665"
                                                                                                                                                                                               /db_xref="taxon:9606"
                                                                                                                                                                                                                        /organism="Homo sapiens"
             /codon_start=1
                                      /note="unnamed protein product"
                                                                                          /note="cloning vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi;
                                                                                             PME18SFL3"
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PRI 31-OCT-2001

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REFERENCE
                                                                                                                                                                                                                                                         KEYWORDS
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                                                                   AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  688 ATCATATGTGGCCATTTGTCAGACAGGT 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               481 atcataggtggccatgtctcagacaggt 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 421 tatcagtcactgaaatcagtggttcaattcctacttctgactggaatgctggtgggaggc 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         328 ACTGCAGCCATTCCCAATCATCGCTGCTGGGCCCCCATCCTTGACAATGACACTGCCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         568 GTGTATGACAGGAGCAACTTCCTTTCTACCATTGTGACTGAGTGGGACCTGGTGTGTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 gtatatgatcaaagctacttcccttcgaccattgtgactaagtgggacctggtatgtgat 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 ctgaatgggactatccacagcacaagtgaggcagacacagaaccctgtgtggatggctgg 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 gctgcagccattcctggtcatcgttgctgggtccacatgctggacaataatactggatct 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 ctggtttttattcttccctctcatgttattaatccctcatatactgctagagaacttt 120
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Direct Submission
Submitted (14-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer
                                                                                                                                                                                                                                                                                                                                     Mus
                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                         Strausberg, R
                                                                                                                                                                                                    Mus musculus
                                                                                                                                                                                                                             house mouse
                                                                                                                                                                                                                                                                                BC021384.1 GI:18204002
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                                                                                                                (bases 1 to 1964)
                                                                                                                                                                                                                                                                                                                             musculus, clone MGC:29260 IMAGE:5064542, mRNA, complete cds.
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SSPRDLFHTPILRKRICVLSFMRYLFTISIFGLSLHLOHLSTNIILLOFLSSALGILI
SVIGHFVLNHMGRRITIQLVLMSLRGIFMLTAVFVPQEMOTLRIIMATLAAALSSLCMC
VSNIHINELLPTTLRATGMGVLAMFGNSGLFLAPLFMLLATYSANLPWIFYGGFSILY
GFSVFLLPETKNQPLPDSIHDVGNDWKESRQAKBEDSIIKVTRF"

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/db_xref="GI:16553417"
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73.6%;
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Pred. No. 4.1e-74;
                                                                                                                                                                                                                                                                                                                                                              1964 bp
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                                                                                                                                                                                                                                                                                                                                                              mRNA
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                                                                                                                                         Murinae; Mus
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181 ggtaatgaaactggaatcctcagtgaagatgccctcttgagaatctctatcccactagac
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                                                                                                                                                                                                                                                                                                                                 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                         1 atggcctttgaggagctcttgagtcaagttggaggccttgggagatttcagatgcttcat 60
                                                                                                                         gctgcagccattcctggtcatcgttgctgggtccacatgctggacaataatactggatct 180
                                                                                       ACTGCAGCCATTCCTAGTCATCGCTGCTGGGTCCCCATCCTTGACAATGACACTGCCTCT
                                                                                                                                                                                                           ATGATATTTGTGTTAATCTGCCATGCCCTGTCGGCTCCTCACACTCTTTTGGAGAACTTC 203
                                                                                                                                                                                                                                                                                                                           ATGGCCTTTCAGGACCTTATAATTCAAATTGGCAGCTTGGGGAGGTTCCAGATTCTTCAC 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 39 Row: n Column: 1
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: nisc_mgc@nhgri.nih.gov
Shevchenko,Y., Wetherby.K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Dietrich,N.I., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaithersburg, Maryland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tissue Procurement: Jeffrey E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Institute,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSHRCWYPILDNDTASDNGSRILSQDDLLRISIPLDSNLRPDKCRRYIQPQWHLLHLN
GTFPTVTEPDTEPCVDGWYXDQSTFLSTTVTQWDLVCGSQALMSVAKFIYMTGIFIGY
IMGGHLSDKFGRKLIFTGSLLKMAITTETCVAFAPSFLIYGSLRFLSGIFSSTLKTNSA
LLILEWTSPKFQALVMALIFIASGVGQTLLGGLAFAFRNWHHLQLALSVPMFLLLIPR
RWLSESARWLLMANKFQKSLKELKKAACVNRIKNSGDALTLEYVKTINKEELEAAQTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PSPLDLFRTPNLRKRICLLSFVRFVSVMSLLGLLINIQYLSNNVFLLQCLYGVVCTPA
NVLGNFSMNYMGRRMTQLIFMSVLGISILAVVFLPQEMQILRVFLSTLGGAISSASIT
STLVHANELVFTIIRATALGVVGIAGSAGGALSPLLMILTTYSASLPWIIYGILPFLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="Unknown (pro
/protein_id="AAH21384."
/db_xref="GI:18204003"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pCMV-SPORT6"
84. .1739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="Kidney, normal.
/clone_lib="NCI_CGAP_Kid14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="MGC:29260 IMAGE:5064542"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               translation="MAFQDLIIQIGSLGRFQILHMIFVLICHALSAPHTLLENFTAAI/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .1964
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73.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 290.4; DB 10; Length Pred. No. 3.4e-73; O; Mismatches 136; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1964;
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REFERENCE
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ORGANISM
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (08-FEB-1999) Gruendemann D., Dept. of Pharmacology,
University of Heidelberg, INF 366, 69120 Heidelberg, 69120, GERMANY
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RANC132859 1911 bp mRNA linear ROD 04-JAN-Rattus norvegicus mRNA for putative integral membrane transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
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AJ132859
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                                                                                                   PERIOD - "MAFQELLNQVGGLGRFQILQMVFVVFTSVIVVPHIIIENFTAAI PSHRCWPFILDNYTVSDNDSRILNQDKLLKISIPLDSHLKLDSCRREAQPQNHLLDLN DFESSITEDDFEDFUNGWVDDSRILNGHSTTVEEWNLVCESQALNSATKLSEMIGAFIGG IVNGLLSDREGRFILKYALLQMAITETCAGFAPNLFIYCSLRFLAGMSLEPITVNIN LLMFEWTSPKFLTMYTVLGSCAGSFGGMILAGLAFQFQNNHLLQLANSVPIFFFLILT RWLPESARWLIVINKPOKGLKELKVAHINGMKKSGDUTIMEVVPRTSMKKELEAAKMR PSPRDLFHTPILRKQIXILSFIRLLFILSGVGVAIHLQHLSNNIELLQILISVSSILF PSPRDLFHTPILRKQTXILSFIRLFFILSGVGVAIHLQHLSNNIELLQILISVSSILF PSYJGHFYLMHIGRRITOMVIMFLRGISILTAIFAFQEMETIFT INAMMAEGLAALSYA ANSLHANELLPTTLRATARGVIGMFGNIGFFPAPLCMMLVSYSPNLPWIFYGGFAILS GFTVLLLPETKNNPLDCTHDVENDKESSRQEMKEDPIIKVTRF" 395 c 397 g 584 t
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121. .1779
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/db_xref="taxon:10116"
/tissue_type="liver"
121...1779
                                                                                                                                                                                                                                                                                                                                     /product="putative integral membrane transport protein"
/protein_id="CAC79639.1"
/db_xref="GI:18076049"
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  35.9%;
73.0%;
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No. 1e-72;
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                       Length 1911;
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                                                                                                                                                                                                gctgcagccattcctggtcatcgttgctgggtccacatgctggacaataatactggatct 180
                                                                                                                                                                                                                                                                   ggtaatgaaactggaatcctcagtgaagatgccctcttgagaatctctatatcccactagac
             atcataggtggccatgtctcagacaggt 508
                                                                      tatcagtcactgaaatcagtggttcaattcctacttctgactggaatgctggtgggaggc 480
                                                                                                  GTATATGACAGGAGCAACTTTCATTCTACCACTGTGACTGAGTGGAACCTGGTGTGAA
                                                                                                              gtatatgatcaaagctacttcccttcgaccattgtgactaagtgggacctggtatgtgat 420
                                                                                                                                                  TTGAATGATACTTTCTCCAGTATAACTGAGCCAGACACTGAGCCCTGTGTGGATGGCTGG
                                                                                                                                                                  ctgaatgggactatccacagcacaagtgaggcagacacagaaccctgtgtgggatggctgg
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ATTGTAAATGGCCTTCTGTCAGACAGGT
                                               TCTCAGGCACTGAATTCTGCCACTAAACTTTCATTTATGATTGGTGCATTTATAGGAGGT
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Search completed: July 1, 2002, 15:41:50 Job time: 10924 sec

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RESULT 15
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Q96DT2;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ORGANIC ANION TRANSPOTER 4 LIKE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "human organic anion transporter 4 similer gene.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB050269; BAB68364.1; -.
SEQUENCE 552 AA; 58729 MW; BE2A3EA23B98B420 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUE-KIDNEY SPECIFIC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    268 KSSEALKILRRVAVFNGKKEEGERLSLEELKLNLQKEISLAKAKYTASDLFRIPMLRR 325
                                                                                                                                               229 RPLVMTLNSLGFSFGHGLTAAVAYGVRDWTLLQLVVSVPFFLCFLYSWWLAESARWLLTT 288
                                                                                                                                                                                                                                                                                                   109 ARPTRSRVWMAGSMTAASSPPQSWQVELVCDSHALKPMAQSIYLAGILVGAAACGPASDR 168
                                                                                                                                                                                                                                                                                                                                        113 TEPCVDG-WVYDQSYFPSTIVTKW--DLVCDYQSLKSVVQFLLLTGMLVGGIIGGHVSDR 169
                                                                     289 GRIDWGIQELWRVAAINGKGAVQDTLTPEVILSAMREELSMGQPPASIGTLIRMPGIRFR 348
                                                                                                         182 NKLDEGLKALRKVARTNGIKNAEETLNIEVVRSTMQEELDAAQTKTTVCDLFRNPSMRKR 241
                                                                                                                                                                                                                           169 FGRRLVLTWSYLQMAVMGTAAAFAPAFPVYCLFRFLLAFAVAGVMMNTGTLLMEWTAARA 228
 349 TCI 351
                                 242 ICI 244
                                                                                                                                                                                                                                                                                                                                                                              61 ASILGSLSPEALLAISIPPGPNQSP-----ISAAASASHSGSSWTPMPRPPAG 108
                                                                                                                                                                                                                                                                                                                                                                                                                61 GNETGILSEDALLRISIPLDSNLRPEKCRRFVHPQWQLLHLNGTIHSTSE-----AD 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MAFSELLDLYGGLGRFQYLQTMALMYSIMWLCTQSMLENFSAAVPSHRCWAPLLDNSTAQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MAFEELLSQVGGLGRFQMLHLVFILPSIMLLIPHILLENFAAAIPGHRCWVHMLDNNTGS 60
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Search completed: July 1, 2002, 11:42:46 Job time: 216 sec

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RESULT 13
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Nigam S.K.;

"Molecular cloning and characterization of NKT, a gene product related to the organic cation transporter family that is almost exclusively expressed in the kidney.";

J. Biol. Chem. 272:6471-6478(1997).
                                                                                                                                                                                                                                                                                                                                                                                                Q61185 PRELIMINARY; PRT; 545 AA.
Q61185; Q61185; Q61185; Q61185; Q61185; Q611000-1996 (TremBLrel. 01, Created)
Q1-NOV-1996 (TremBLrel. 01, Last sequence update)
Q1-DEC-2001 (TremBLrel. 19, Last annotation update)
KIDNEY-SPECIFIC TRANSPORT PROTEIN.
                                                                                                                                                        MEDLINE-97197822; PubMed-9045672;
Lopez-Nieto C.E., You G., Bush K.T., Barros E.J.,
                                                                                                                                                                                                                      STRAIN-BALB/C;
                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  354 L 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             I 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEGIKALRKVARTNGIKNAEETLNIEVVRSTMQEELDAAQTKTTVCDLFRNPSMRKR-IC 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VGTTTGYCYTLGQLILVLLAYFIRDWRWLTLAVSLPFYVFFLIAWWFHESSRWLALSNRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LQECSDGWSYNSTVRSSTIISEWHLVCDMHSFKQMGQTIYMGGVLVGALLFGGLSDRYGR 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -EPCVDGWVYDQSYFPSTIVTKWDLVCDYQSLKSVVQFLLLTGMLVGGIIGGHVSDR--- 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GNETGILSEDALLRISIPLDSNLRPEKCRRFVHPQWQLLHLNGTIHSTSEADT----- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAFEELLSQVGGLGRFQMLHLVFILPSLMLLIPHILLENFAAAIPGHRCWVHMLDNNTGS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RILLLISNLLMAVSGTCAAFSSSFSLFCVFRFGCGLALSGLGLNTFSLIVEWIPTRIRTA 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LSQARLSLEESLL-ITVPLDGAGKPQRCQRYAAPQWHLLGKNGTSGSGDLADATESMDAA 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 439; DB 13;
Pred. No. 5.4e-34;
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N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
TLINKED (GLCNAC. . .) (POTENTIAL);
7DC1A67F32801D2D CRC64;
                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
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                                                                                                                                                              Beier D.R.,
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                              Q96TC1 PRELIMINARY; PRT; 542 AA.
Q96TC1;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases EMBL; AB042505; BAB47393.1; -.
                                                                                                                                                                                                                                            Cha S., Sekine T., Kanai Y., Endou H.; "Molecular cloning and characterization of human organic transporter 3.";
                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                    HOAT3
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U52842; AAC53112.1; -.
MGD; MGI:892001; S1c22a6.
InterPro; IPR003662; sub_transporter.
Pfam; PF00083; sugar_tr; 1.
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    61 V----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   224 YSLGQFLLAGIAYAVPHWRHLQLAVSVPFFVAFIYSWFFIESARWYSSSGRLDLTLRALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              164 LQTAVSGTCAAYAPNYTVYCIFRLLSGMSLASIAINCMTLNMEWMPIHTRAYVGTLIGYV 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
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                          VHMLDNNTGSGNETGILSEDALLRISIPLDSNLRPEKCRRFVHPQWQLLHLNGTIHSTSE 110
                                                          MTFSEILDRVGSMGHFQFLHVAILGLPILNMANHNLLQIFTAATPVHHCRPPHNASTGPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RVARINGKQEEGAKLSIEVLQTSLQKELTLNKGQASAMELLRCPTLRRLFLCLSML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VYDNSTFPSTIVTEWNLVCSHRAFRQLAQSLFMVGVLLGAMMFGYLADRLGRRKVLILNY 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GNETGILSEDALLRISIPLDSNLRPEKCRRFVHPQWQLLHLNGTIHSTSEADTEPCVDGW 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AN----LSKDGGLEARLPLDKQGRPESCLRFPFPH-----NGT-EANGTGVTEPCLDGW 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAFNDLLKQVGGVGRFQLIQVTMVVAPLLLMASHNTLQNFTAAIPAHHC-----RPPAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            102;
                                                                                                                                                                                                  542 AA;
                                                                                                                         Conservative
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                                                                                                                                                                                               **/393.1; -. 59857 MW; 5053B36439554CCC CRC64;
                                                                                                                                    27.8%;
25.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31.2%; Score 438.5; DB 11;
28.7%; Pred. No. 5.8e-34;
29. Mismatches 77;
                                                                                                                         46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----VESARWLIITNKLDEGLKALR 192
                                                                                                                                   Score 390.5; DB 4
Pred. No. 2.6e-29;
--LPMGPNGKPERCLRFVHPP----NASLPNDTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CD3B762E5984933A CRC64;
                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----WL-----
                                                                                                                                                  DB 4; Length 542;
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                                                                                                                                Q9TSY7
Q9TSY7;
Q1-MAY-2000
                                                                01-MAY-2000 (TYEMBLIFE). 13, Created)
01-MAY-2000 (TYEMBLIFE). 13, Last sequence update)
01-DEC-2001 (TYEMBLIFE). 19, Last annotation update)
RENAL ORGANIC ANION TRANSPORTER 1 (RBOAT1).
      Eukaryota;
                           Oryctolagus
                                                  ROAT1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organic anion transporter. J. Biol. Chem. 272:18526-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          170
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                                                                                                                                                                                                                                                                                        290 RVARINGKQEEGAKLSIEVLRTSLQKELTLSKGQASAMELLRCPTLRHLFLCLSML
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biol. Chem. 272:18526-18529(1997).

FUNCTION: MEDIATES THE NA(+)-INDEPENDENT TRANSPORT OF ORGANIC ANIONS SUCH AS CYCLIC NUCLEOTIDES, PROSTAGLANDIN E2 AND URIC & SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. BASOLATERAL MEMBRANE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE SPECIFICITY: STRONG EXPRESSION IN KIDNEY. VERY WEAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTM: GLYCOSYLATED (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SKELETAL MUSCLE, SMALL INTESTINE, LARGE INTESTIEST IN THE PROXIMAL TUBULE IN THE KIDNEY.
                                                                                                                                                                                                                                                                                                                                    KVARTNGIKNAEETLNIEVVRSTMQEELDAAQTKTTVCDLFRNPSMRKRICILVFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LQTAVSGTCAAYAPNYTVYCVFRLLSGMSLASIAINCMTLNVEWMPIHTRAYVGTLIGYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VYDNSTFPSTIVTEWNLVCSHRAFRQLAQSLYMVGVLLGAMVFGYLADRLGRRKVLILNY 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VYDQSYFPSTIVTKWDLVCDYQSLKSVVQFLLLTGMLVGGIIGGHVSDR-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AN----LSKDGGLEAWLPLDKQGQPESCLRFTSPQWGPPFYNGT-EANGTRVTEPCIDGW 109
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PF00083; sugar_tr; 1.
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    Metazoa;
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                           cuniculus (Rabbit)
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                                                                                                                                                                              PRELIMINARY;
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29.2%;
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LL INTESTINE, LARGE INT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52;
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Pred. No. 8.5
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N-LINKED (GLCNAC. ...
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Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                 551
                                                                                                                                                                                                                                                                                                                                                                                                                       -----VESARWLIITNKLDEGLKALR 192
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(POTENTIAL).
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    Euteleostomi;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                         057379;
                                                                                        "Expression cloning and characterization transporter from winter flounder."; FEBS Lett. 417:287-291(1997).
                                                                                                                                                                                                                                              Pseudopleuronecta americanus (Winter flounder).

Eukaryota; Metazoa; Chordata; Craniata; Purtebrata; Euteleostom Actinopterygii; Meleostei; Euteleostei; Neoteleost Actanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
                                                                                                                                                                                                                                                                                                            01-JUN-1998 (TremBLrel. 06, Crea 01-JUN-1998 (TremBLrel. 17, Last 01-JUN-2001 (TremBLrel. 17, Last RENAL ORGANIC ANION TRANSFORTER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bahn A., Knabe M., Hillemann A., Burckhardt G.; Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases. -:- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY -:- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY EMBL; AJ242871; CAB62587.1; ...
                                                                                                                                                                         TISSUE=KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
TISSUE=KIDNEY CORTEX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9986;
                                                                                                                                       Wolff N.A., Werner A., Burkhardt S., Burckhardt G.;
                                                                                                                                                       MEDLINE=98072393; PubMed=9409735;
                                                                                                                                                                                   SEQUENCE FROM N.A., AND FUNCTION
                                                                                                                                                                                                                                   Pleuronectoidei; Pleuronectidae; Pseudopleuronectes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00083; sugar_tr;
                                                                                                                                                                                                                   NCBI_TaxID=8265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     193
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                                MEMBRANE (POTENTIAL).
                                         ANIONS SUCH AS P-AMINOHIPPURATE SUBCELLULAR LOCATION: INTEGRAL 1
                                                                             FUNCTION: MEDIATES THE NA(+)-INDEPENDENT TRANSPORT OF ORGANIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MAFEELLSQVGGLGRFQMLHLVFILPSLMLLIPHILLENFAAAIPGHRCWVHMLDNNTGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KVARTNGIKNAEETLNIEVVRSTMQEELDAAQTKTTVCDLFRNPSMRKRICILVFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YSTGQFLLAGVAYAVPHWRYLQLLVSVPFFAFFVYSWFFIESARWYSTPGRLDLTLKALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LQTAVSGTCAAFSPNFTVYCTFRLLSGMSLAGIALNCMTLNVEWMPIHTRAYVGTLAGYV 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IYDNSTFPSTIVTEWDLVCSHRALRQLGQSLYMAGVLIGAMVFGYLADRLGRRKVLILNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----LSKDGGLQAWLPQDTQGRPKSCLRFTSPQERPPFLNGT-EANGTGTTEPCTDGW 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GNETGILSEDALLRISIPLDSNLRPEKCRRFVHPQWQLLHLNGTIHSTSEADTEPCVDGW 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAFNDLLKQVGGVGRFQRIQVTLVVLPLLLMASHNTLQNFTAAIPPHHCRPPAHAN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            105;
                GLYCOSYLATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR003662; sub_transporter.
                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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 BELONGS
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            (BY SIMILARITY)
TO
THE
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                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                          Last annotation
                                                                                                                                                                                                                                                                                                                                            Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 449.5; DB (
Pred. No. 5.1e-35;
                                                                                                                                                                                                                                                                                                                                                                                         PRT;
SLC21 FAMILY
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                                                MEMBRANE
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                                                                                                                                                                                                                                                                Euteleostei; Neoteleostei;
                                                                                                                                                                                                                                                                             Vertebrata; Euteleostomi;
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                                                                                                                        a renal organic anion
 OF TRANSPORTERS
                                              PROTEIN.
                                                                                                                                                                                                                                                                                                                            update)
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transporter gene (hoatl).";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: MEDIATES THE NA(+)-INDEPENDENT TRANSPORT OF ORGANIC ANIONS SUCH AS P-AMINOHIPPURATE AND ALPHA-KETOGLUTARATE.
-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. BASOLATERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lu R., Chan B.S., Schuster V.L.;
Cloning of the human kidney PAH transporter: narrow substrate specificity and regulation by protein kinase C.";
Am. J. Physiol. 276:F295-F303(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-99160894; PubMed=10049739; Race J.E., Grassl S.M., Williams W.J., Holtzman E.J.; "Molecular cloning and characterization of two novel human renal organic anion transporters (hOATI and hOATI).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reid G., Wolff N.A., Dautzenberg F.M., Burckhardt G.; "Cloning of a human renal p-aminohippurate transporter, Kidney Blood Press. Res. 21:233-237(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606; [1]
                                                                                                                                                                                                                                                                                                                                                                                                                    Bahn A., Prawitt D., Reid G., Enklaar T., Wolff N.A., Hillemann A., Godehardt S., Buttler D., Knabe M., Schulten H.J., Gunawan B., Fuezesi L., Zabel B., Burckhardt G.; "Genomic cloning and characterization of the human renal organic anion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hosoyamada M., Sekine T., Kanai Y., Endou H.; o "Molecular cloning and functional expression o organic anion transporter from human kidney."; Am. J. Physiol. 276:F122-F128(1999).
                            Pfam; PF00083;
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                                                      TISSUE SPECIFICITY: STRONGLY EXPRESSED IN KIDNEY. ALSO DETECTED BY ALTERNATIVE SPLICING.
BRAIN AND AT LOW LEVELS, IN SKELETAL MUSCLE AND PLACENTA. NOT EXPRESSED IN HEART, LUNG, LIVER, PANCREAS, COLON, THYNUS, SMALL INTESTINE OR PERIPHERAL BLOOD LEUKOCYTES. IN THE KIDNEY, STRONGLY EXPRESSED IN PROXIMAL TUBULE CELLS.
                                                                                                                                                                                                                                                                         MEMBRANE (POTENTIAL).

ALTERNATIVE PRODUCTS: 2 ISOFORMS; ISOFORM HOAT1-1 (SHOWN HERE)
AND ISOFORM HOAT1-2; ARE PRODUCED BY ALTERNATIVE SPLICING.

TISSUE SPECIFICITY: STRONGLY EXPRESSED IN KIDNEY. ALSO DETECTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antiviral nucleotide analogs cidofovir and adefovir are novel trates for human and rat renal organic anion transporter 1."; Pharmacol. 56:570-580(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T., Lin D.C., Pritchard J.B., Fuller M.D., Mendel D.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biophys. Res. Commun. 255:508-514(1999).
                            IPR003662; sub_transporter.
0083; sugar_tr; 1.
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             Transport; Alternative
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           splicing;
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O1-JAN-1998 (TrEMBLrel. 0
O1-JAN-1998 (TrEMBLrel. 0
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
RENAL ORGANIC ANION TRANSPORT PROTEIN 1.
                                                         "Sweet D.H., Wolff N.A., Pritchard J.B.;
"Expression cloning and characterization o organic anion transporter in rat kidney.";
J. Biol. Chem. 272:30088-30095(1997).
MEDLINE=97373539; PubMed=9228014; Sekine T., Watanabe N., Hosoyamad
                                                                                                         MEDLINE=98043701; PubMed=9374486;
                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
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                        STRAIN-SPRAGUE-DAWLEY;
                                  SEQUENCE FROM N.A., FUNCTION,
                                                                                                                     TISSUE=KIDNEY;
                                                                                                                               SEQUENCE FROM N.A.,
                                                                                                                                                       NCBI_TaxID=10116;
                                                                                                                                                                                          Rattus norvegicus (Rat)
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L -> F (IN REF. 2).
YM; 74AD3EA2678032E4 CRC64;
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Sciurognathi; Muridae;
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Bahn A., Prawitt D., Buttler D., Reid G., Enklaar T., Wolff N.A.,
Ebbinghaus C., Hillemann A., Schulten H.J., Gunawan B., Fuezesi L.,
Zabel B., Burckhardt G.,
"Genomic structure and in Vivo expression of the human organic anion
transporter 1 (hOarl) gene.";
Biochem. Biophys. Res. Commun. 275:623-630(2000).
1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
EMBL. AJZ51529; CAB94830.1; -.
EMBL: AJZ51529; CAB94830.1; -.
230 YSLGQFILAGVAYAVPHWRHLQLLVSAPFFAFFIYSWFFIESARWHSSSGRLDLTLRALQ 289
                                                               172 -----VESARWLIITNKLDEGLKALR 192
                                                                                                                                  170 LQTAVSGTCAAFADNFPIYCAFRLLSGMALAGISLNCMTLNVEWMPIHTRACVGTLIGYV 229
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Q9NOC2;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE ORGANIC ANION TRANSPORTER.
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Rukarvota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR003662; sub_transporter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     506 AA; 55858 MW; D8EBAE8All3E6C5E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32.6%; Score 458.5; DB 4; Length 506; 29.2%; Pred. No. 6.1e-36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                        095742 PRELIMINARY; 977, 563 AA. 095742; 095187; 09UBC8; 09UBC8; 09UBC8; 01-MAY-1999 (TremBLrel. 10, Created) 01-MAY-1999 (TremBLrel. 10, Last sequence update) 01-JUN-2001 (TremBLrel. 17, Last annotation update) RENAL ORGANIC ANION TRANSPORT PROTEIN 1.
                Eukaryota; Metazoa;
                                Homo sapiens (Human)
                                                    SLC22A6 OR OAT1 OR ROAT1.
                                                                                                                                                                                                                                                  290 RVARINGKREEGAKLSMEVLRASLQKELTMGKGQASAMELLRCPTLRHLFLCLSML
                                                                                                                                                                                                                                                                                     193 KVARTINGIKNAEETLNIEVVRSTMQEELDAAQTKTTVCDLFRNPSMRKRICILVFL 248
                                                                                                                                                                                                                                                                                                                           230 YSLGQFILLAGVAYAVPHWRHLQLLVSAPFFAFFIYSWFFIESARWHSSSGRLDLTLRALQ 289
                                                                                                                                                                                                                                                                                                                                                                                                  170 LQTAVSGTCAAFAPNFPIYCAFRLLSGMALAGISLNCMTLNVEWMPIHTRĄCVGTLIGYV 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transporter 1 (hOAT1) gene ;
Biochem. Biophys. Res. Commun. 275:623-630(2000).

EMBL; AJ271205; CAB97249.1; -
SEQUENCE 519 AA; 57357 MW; E1748C6F9E2002F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9NOA6 PRELIMINARY; PRT; 519 AA.
09NOA6;
01-OCT-2000 (TremBirel. 15, Created)
01-OCT-2000 (TremBirel. 15, Last sequence update)
01-DEC-2001 (TremBirel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110 IYDNSTFPSTIVTEWDLVCSHRALRQLAQSLYMVGVLLGAMVFGYLADRLGRRKVLILNY 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bahn A., Prawitt D., Buttler D., Reid G., Enklaar T., Wolff N.A., Ebbinghaus C., Hillemann A., Schulten H.J., Gunawan B., Fuezesi L., Zabel B., Burckhardt G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 VYDQSYFPSTIVTKWDLVCDYQSLKSVVQFLLLTGMLVGGIIGGHVSDR------ 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20422308; PubMed=10964714;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55 AN----LSKNGGLEVWLPRDRQGQPESCLRFTSPQWGLPFLNGT-EANGTGATEPCTDGW 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GNETGILSEDALLRISIPLDSNLRPEKCRRFVHPOWQLLHLNGTIHSTSEADTEPCVDGW 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               290 RVARINGKREEGAKLSMEVLRASLQKELTMGKGQASAMELLRCPTLRHLFLCLSML 345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MAFNDLLQQVGGVGRFQQIQVTLVVLPLLLMASHNTLQNFTAAIPTHHC-----RPPAD 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MAFEELLSQVGGLGREQMLHLVFILPSLMLLIPHILLENFAAAIPGHRCWVHMLDNNTGS 60
Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                           ------ 171
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"Sequencing of human neurexin II gene.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AC044790; AAK68156.1; -.
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SEQUENCE FROM N.A.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ORGANIC ANION TRANSPORTER 4 (OAT4)
HOAT4 OR OAT4.
Rowen L., Madan A., Qin S., Baradarani L., Birditt B., I Burke J., Dors M., Fleetwood P., Kaur A., Madan A., Nesl Pate D., Hood L.;
"Sequencing of human neurexin II gene.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB026116; BAA95316.1;
EMBL; AC044790; AAK68155.1;
EMBL; AC044790; AAK68155.1;
SEQUENCE 550 AA; 59971 MW; 233BE6C4A520E58A CRC64;
                                                                                                                                                                                                                                                                                                                                            Cha S.H., Sekine T., Kusuhara H., Yu E., Kim J.Y., Kim D.K., Sugiyama Y., Kanai Y., Endou H.;
"Molecular cloning and characterization of multispecific organic anion transporter 4 expressed in the placenta.";
J. Biol. Chem. 275:4507-4512(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20127945; PubMed=10660625;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-KIDNEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   193 KVARTNGIKNAEETLNIEVVRSTMQEELDAAQTKTTVCDLFRNPSMRKRICI 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 FSFGHGLTAAVAYGVRDWTLLQLVVSVPFFLCFLYSWWLAESARWLLTTGRLDWGLQELW 300
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37.8%; Pred. No. 1e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                               Birditt B., Bloom S.,
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                                                                                            Matches 120;
                                                                                                             Query Match
Best Local :
                                                                                                                                                                                                                                                                                             Mori K., Ogawa Y., Ebihara K., Aoki T., Tamura N., Sugawara A., Kuwahara T., Ozaki S., Mukoyama M., Tashiro K., Tanaka I., Nakao K.; "Kidney-specific expression of a novel mouse organic cation transporter-like protein."; FEBS Lett. 417:371-374(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-1998 (TrEMBLrel.
01-JUN-1998 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   054778;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 176 CCLQLAVAGTSTIFAPTFVIYCGLRFVAAFGMAGIFLSSLTLMVEWTTTSRRAVTMTVVG 235
                                                                                                                                                                                                       -i- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
EMBL; AB005451; BAA23875.1; --
MGD; MGI:1155269; S1c22a12.
InterPro; IPR003662; sub_transporter.
pfam; PF00083; sugar_tr; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                                          Transmembrane.
SEQUENCE 553
                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98072412; PubMed=9409754;
                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-KIDNEY
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          191 LRKVARTNGIKNAEETLNIEVVRSTMQEELDAAQTKTTVCDLFRNPSMRKRICILV 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      236 CAFSAGQAALGGLAFALRDWRTLQLAASVPFFAISLISWWLPESARWLIIKGKPDQALQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MAFEELLSQVGGLGRFQMLH-LVFILPSLMLLIP-HILLENFAAAIPGHRCWVHMLDNNT 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                             1 MAFEELLSQVGGLGRFQMLHLVFILPSLMLLIPHILLENFAAAIPGHRCWVHMLDNNTGS 60
                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAFSKLLEQAGGVGLFQTLQVLTFILPCLM--IPSQMLLENFSAAIPGHRCWTHMLDN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GWYYDQSYFPSTIVTKWDLYCDYQSLKSVVQFLLLTGMLYGGIIGGHVSDR----- 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GSAVSTN-MTPKALLTISIPPGPNQGPHQCRRFRQPQWQLLDPNATATSWSEADTEPCVD 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSGNETGILSEDALLRISIPLDSNLRPEKCRRFVHPQWQLLHLNGTIHSTSEADTEPCVD 118
GNETGILSEDALLRISIPLDSNLRPEKCRRFVHPQWQLLHLNGTIHSTSEADTEPCVDGW 120
                               MAFPELLDRYGGLGRFQLFQTVALVTPILWYTTQNMLENFSAAVPHHRCWVPLLDNSTSQ 60
                                                                                                              Similarity
                                                                                                                                                                          553 AA; 60160 MW; D991F5F74A39BBBF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42.1%; Score 592; DB 4; Length 550;
40.2%; Pred. No. 7.7e-49;
ative 28; Mismatches 69; Indels 1
                                                                                                              39.2%; Score 551; DB 11; Length 553; 34.1%; Pred. No. 7.3e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06,
19,
                                                                                                   38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          553 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69; Indels 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -WLVESARWLIITNKLDEGLKA 190
                                                                                                      86;
                                                                                                        Indels 108;
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61 ASIPGDLGPDVLLAVSIPPGPDQQPHQCLRFRQPQWQLTESNATATNWSDAATEPCEDGW 120

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RA Matsumoto K., Hirano M., Sano S., Nomura R., Yoshikawa Y.,
RA Matsumura Y., Moriya S., Chiba E., Momiyama H., Onogawa S.,
RA Kaeriyama S., Satoh N., Matsunawa H., Takahashi E., Kataoka R.,
RA Kuga N., Kuroda A., Satoh I., Kamata K., Takami S., Terashima Y.,
RA Watanabe M., Sugiyama T., Irie R., Otsuki T., Sato H., Ota T.,
RA Watanabe M., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K.,
RA Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K.,
RA Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y.,
RA Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Murakawa K.,
RA Kanehori K., Takahashi-Fujii A., Oshima A., Suyiyama A., Kawakami B.,
RA Kanehori K., Takahashi-Fujii A., Oshima A., Suyiyama A., Kawakami B.,
RA Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.,
RI Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL, AK057654, BAB71543.1; -.

BOR SEQUENCE 552 AA, 62140 MW; 39A831COFD26CA68 CRC64;
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Q96LX3
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01-DEC-2001 (TremBlrel. 19, Last sequence update)
01-DEC-2001 (TremBlrel. 19, Last sequence update)
01-DEC-2001 (TremBlrel. 19, Last annotation update)
CDNA FLJ33092 FIS, CLONE TRACH2000665, MODERATELY SIMILAR TO RATTUS
NORVEGICUS PUTATIVE INTEGRAL MEMBRANE TRANSPORT PROTEIN (USTIR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q96LX3;
                                                                                                     169
181 LQFAITETCVAFAPSFFIYCLLRFLAGMSVEPISVNSHLLMLEWTSPKFLGMVAVLTSCA 240
                                                                                                                                                                                                                      121 VYDQSYFPSTIVTKWDLVCDYQSLKSVVQFLLLTGMLVGGIIGGHVSD------ 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FISSUE-TRACHEA;
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                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 55.0%; Score 773; DB 4; Length 552; Local Similarity 43.4%; Pred. No. 2.2e-66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 KVAHINGMKNSTDVLTIEVVRTIMKEELEASQTKSSLWDLFRTPNLRKRICLLSLVR 357
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                                                                                                                                                                                                                                                                                                DNGSRILSQDDLLRISIPLDSNLRLDKCRRFAQPQWHLLHLNGTFSNETEPDTEPCVDGW 120
                                                                                                                                                                                                                                                                                                                                       GNETGILSEDALLRISIPLDSNLRPEKCRREVHPQWQLLHLNGTIHSTSEADTEPCVDGW 120
                                                                                                                                                                                                                                                                                                                                                                                                                                            MARQELLNQVGSLGREQILQISFVLFLVGLVVPHITMENFTAAIPNHRCWAPILDNDTAS 60
                                                                                                                                                   VYDRSNFLSTIVTEWDLVCESQALNSVAKFSFMIGLFIGAIICGHLSDRFGRKFILTCAL 180
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RESULT
Q96S37
ID Q9
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COC ECC
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Q91WJ2
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Best Local
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                                                                                   Q96S37;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
NCBI_TaxID=9606;
               Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
Strausberg R.;
Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC014805; AAH14805.1; -.
SEOUENCE 552 AA; 61380 MW; F5D2498FC673E8FC CRC64;
                                                     Homo sapiens (Human)
                                                                                                                                                                       Q96S37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TremBLrel. 19, Created)
01-DEC-2001 (TremBLrel. 19, Last sequence update)
01-DEC-2001 (TremBLrel. 19, Last annotation update)
01-DEC-2001 (TremBLrel. 19, Last annotation update)
SIMILAR TO SOLUTE CARRIER FAMILY 22 (ORGANIC CATION TRANSPORTER)-LIKE
                                                                                                                                                                                                                                                                  301
                                                                                                                                                                                                                                                                              193 KVARTNGIKNAEETLNIEVVRSTMQEELDAAQTKTTVCDLFRNPSMRKRICILVFLR 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                                                          181 LQMAITGTCTALAPTFFIYCLLRFLTGLCIIPINTNSVLLMLEWTSPKTQALVTTLSMSS 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                          169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                241 HHFGGLILAGLAFAFQNWHHLQLAISVPIFVLLIPTRWLTESARWLIVTNKPQKALQELR 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 VYDQSYFPSTIVTKWDLVCDYQSLKSVVQFLLLTGMLVGGIIGGHVSD------ 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 NNNSGILSQDDLLRISIPLDSNLRPEKCRRFVQPQWHLLQFNGSFSNMTEPDTEPCMDGW 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GNETGILSEDALLRISIPLDSNLRÞEKCRRFVHÞQWQLLHLNGTIHSTSEADTEPCVDGW 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 KVAHMNGMKNSGNTLTMEVVEASMKNELEAAKRKSSPRDLFHTPILRKRICVLSFMR 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 53.4%; Score 751; DB 1
Local Similarity 41.5%; Pred. No. 3e-64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MAFEELLSQVGGLGRFQMLHLVFILPSLMLLIPHILLENFAAAIPGHRCWVHMLDNNTGS 60
                                                                                                                                                                                                           4
                                                                                                                                                                                                                                                           KVASKNGIKNSEDVLTMEVVRTIMKDEIAIPRTKPSLRDLFHMPNLRKRLCLLCLLR 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VYDQRTFLSTTVTEWNLVCGSQELNSVAKF1FL1GVLAGHFVGGHLSDKFGRKLLFRCAL 180
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                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44; Mismatches
                                                                                     Last sequence update)
Last annotation update)
           Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                        -----RWLVESARWLIITNKLDEGLKALR 192
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Perfect score:
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Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sp_organelle:*
sp_phage:*
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sp_bacteria:*
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sp_archeap:*
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sp_rvirus:*
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sp_virus:*
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O61185 mus musculu
O96tc1 homo sapien
O96dt2 homo sapien
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Q96s37 homo sapien
Q9nsa0 homo sapien
Q54778 mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                    070609 rattus norv
Q961x3 homo sapien
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Q9nqa6 homo sapien
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	Ol4546 homo sapien		Q9h015 homo sapien			nomo	omon	റ			Q95r48 drosophila	002270 caenorhabdi		v	rat:		dros		Q96135 drosopnila	drosopni			nomo	nomo	0 ratt	2 mus muscul	ratt	rattus	088909 mus musculu

## ALIGNMENTS

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RESULT
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                                                                                                                                                             В
                                 å
                                                                        Query Match 58.2%; Score 818; DB 11; Best Local Similarity 45.9%; Pred. No. 9.5e-71; Matches 164; Conservative 40; Mismatches 45;
                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O70609 PRELIMINARY; PRT; 552 AA.
O70609;
O1-AUG-1998 (TrEMBLrel. 07, Created)
O1-AUG-1998 (TrEMBLrel. 07, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                       "Molecular cloning and characterization of two novel transport proteins from rat kidney.";
FEBS Lett. 425:79-86(1998).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
EMBL; Y09945; CAA71076.1; -.
InterPro; IPR003662; sub_transporter.
Pfam; PF00083; sugar_tr; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PUTATIVE INTEGRAL MEMBRANE TRANSPORT PROTEIN.
                                                                                                                                                           Transmembrane.
SEQUENCE 552 AA; 61476 MW; F47FB42B41F5C4AF CRC64;
                                                                                                                                                                                                                                                                                                                                                        MEDLINE-98200080; PubMed-9541011;
Schoemig E., Spitzenberger F., Engelhardt M., Martel F., Oerding N.,
                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                           Gruendemann D.;
                    MAFEELLSQVGGLGRFQMLHLVFILPSLMLLIPHILLENFAAAIPGHRCWVHMLDNNTGS 60
MAFQDLLNQVGSLGRFQILOMTFILIFNIIISPHSLLENFTAVIPNHRCWVPILDNDTVS 60
                                                                      164;
                                                                      Conservative
                                                                      40;
                                                                           45;
                                                                                                         Length 552;
                                                                           Indels 108;
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